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5.1.6 Compugen Ltd.		October 14, 2005, 15:51:19; Search time 38.4375 Seconds (without alignments) 50.310 Million cell updates/sec	
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	OM protein - protein search, using sw model	;005, 15:51:19 ; (v) 5(1-10
Copyright	rotein search,	October 14, 2	US-10-614-959-10 29 1 TYAMH 5
	OM protein - p	Run on:	Title: Perfect score: Sequence:

	(without alignment 50.310 Million cel
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2105692 seqs, 386760381 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

10000	Description	Aay79068 Anti-fact		4		7 HCV E	9 HCV E1	7 Protein	~	~			~	-	Α.	l Asp		v		'n	Aam73798 Human bon	Human	6 Human	5 Human	· œ	Human	
SUMMARIES NA ID	ij	3 AAY79068	3 AAB14789	3 AAB14784	4 AAG65570	5 ABG76537	S ABG76559	6 ABU24807	7 ABO77482	8 ADN27332	4 AAG72483		8 ADR10293	•		3 AAB14781	•		4 ABB40299		4 AAM73798	4 AAM61093	4 ABG55546	5 ABG43685	4 AAU18208	•	
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& Query Match		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	თ	89.7	σ	o,	ę,	89.7	89.7	89.7	89.7	
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ADC25346 ABG68752 ABP01222 ABP01222 ADE08119 ADE08119 ADE55112 ADE55112 ADE55112 ADE55112 ADE59014 AAC91423 AAC90014 AAC90013 AAC9003 ADC47242 ADC47242	ADES7190
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ALIGNMENTS

Anti-factor IX/IXa antibody H chain V domain CDR1 amino acid sequence

Complementarity determining region 1; CDR1; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastesis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC.

Kirchhofer D; Hass PE, Judice JK,

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

This sequence represents a complementarity determining region 1 (CDR1) of the heavy chain variable domain of a human anti-factor IX/Ixa Gla domain antibody. Pactor IXA/Ixa a vitamin K dependent plasma serine procease that participates in the blood coaqulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

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Aspergillus oryzae KBN616 and Aspergillus sojae BA-104 respectively which have molecular weights of approximately 73 kD (as determined by gel filtration). The enzymes have an optimum temperature of approximately 50 degrees Celsius, and an optimum pH of about 8.5. The glutaminases catalyse the conversion of L-glutamine to L-glutamic acid, and may be used in the production of fermented foodstuffs such as soy sauce and miso. Sequences AABA1787-1814789 represent fragments of Aspergillus oryzae KBN616 glutaminase which were used as the basis for the design of Aegenerate PCR primers AAA72206, AAA72207 and AAA72209. These primers were used in the isolation of genomic DNA encoding Aspergillus oryzae
                                                                                                                                                                                                                                                                 ö
           the treatment or prophylaxis of thrombotic or coaguiopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarttion, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary angioplasty (PTCA), stroke, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
platelets. Compositions comprising the antibodies are used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glutaminase, Aspergillus oryzae KBN616; glutamic acid synthesis;
fermentation; foodstuff production; miso; soy sauce; peptide fragment;
                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus oryzae KBN616 glutaminase peptide, SEQ ID NO:12.
                                                                                                                                                                                                                           ; Score 29; DB 3; Length 5;
; Pred. No. 1.8e+06;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A new glutaminase and its preparation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 25; 27pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                AAB14789 standard; peptide; 7 AA.
                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergillus oryzae.
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR primer design.
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                                                                                                                                                                                                                                                                                                        1 TYAMH 5
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                                                                                                                                                                                               Sequence 5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB14789;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                 AAB14789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aspergillus oryzae KBNG16 and Aspergillus sojae BA-104 respectively which have molecular weights of approximately 73 kD (as determined by gel filtration). The enzymes have an optimum temperature of approximately 50 degrees Celsius, and an optimum pH of about 8.5. The glutaminases catalyse the conversion of L-glutamine to L-glutamic acid, and may be used in the production of fermented foodsruffs such as soy sauce and miso. Sequences AAB14784-B14786 represent the N-terminal sequences determined for three V8 protease fragments (P1-P3) of Aspergillus oryzae KBN616 glutaminase in an exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to two novel glutaminases (AAB14781, AAB14782)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
                                                                                                            SEQ ID NO:6.
                                                                                                                                          Glutaminase; Aspergillus oryzae KBN616; glutamic acid synthesis;
fermentation; foodstuff production; miso; soy sauce;
V8 protease digestion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 29; DB 3; Length 12; 100.0%; Pred. No. 6.5; ive 0; Mismatches 0; Indels
                                                                                                               Aspergillus oryzae KBN616 glutaminase peptide fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene library; immunoglobulin; antibody library; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of protein seq Id No. 95.
                                                                                                                                                                                                                                                                                                                                                                                                                                       A new glutaminase and its preparation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG65570 standard; protein; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 9; 27pp; Japanese.
                         AAB14784 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                 98JP-00347127.
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                                                                                    06-DEC-2000 (first entry)
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-477931/42
                                                                                                                                                                                                          Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 TYAMH 11
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                                                       AAB14784;
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RESULT 3
               AAB14784
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100.0%; Score 29; DB 3; Length 7; 100.0%; Pred. No. 1.8e+06; cive 0; Mismatches 0; Indels

5; Conservative

Query Match Best Local Similarity Matches 5; Conserv

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05-NOV-2002
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                                                                                                                                                                                                                                                       The invention relates to producing gene libraries, comprising immunoglobulin light and heavy variable region. The method involves selecting light chain that binds with the heavy chain product to produce a functional conformation, producing a gene library comprising a collection of these light chain variable genes, and combining with gene library of heavy chain variable genes. The method is used for production of gene and antibody libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; HCV; hepatitis C virus; El antigen; monoclonal antibody; vaccine; hepatotropic; Fab; hypervariable region; E2 antigen; antibody.
                                                                                                                                                                                  Producing gene libraries and antibody libraries, involves selecting a
light chain that binds to a heavy chain product to produce a functional
formation, and producing a gene library of the light chain variable
                                                                                                                           Takahashi M;
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100.0%; Pred. No. 72;
tive 0; Mismatches 0; Indels
                                                                                                                         Shinohara M,
                                                                                                                         Iba Y, Morino K,
                                                                                                    (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HCV El antigen monoclonal antibody #25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG76537 standard; protein; 121 AA.
                                                                                                                                                                                                                                       Examples; p 171; 181pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KARO-) KAROLINSKA INNOVATIONS
                                                           22-FEB-2001; 2001WO-JP001298
                                                                               22-FEB-2000; 2000JP-00050543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Persson MAA;
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                                                                                                                       Akahori Y,
                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
                                                                                                                                 Shiraki K;
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Best Local Similarity
Matches 5; Conserv
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                     WO200162907-A1
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  Homo sapiens
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                                                                                                                        Киговама У,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                        30-AUG-2001
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                                                                                                                                   Okuno Y,
                                                                                                                                                                                                                   regions.
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AC ABG7
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Vaccine comprising a human monoclonal antibody against hepatitis C virus (HCV) El or E2 antigen, useful for treating or preventing HCV infection.
                                                                                                                                                                                  The invention relates to a human monoclonal antibody or its antigen binding fragments, which exhibit immunological binding affinity for a hepatitis C virus (HCV) B1 antigen, comprising an amino acid sequence homologous to the binding portion of a human antibody Fab molecule from combinatorial antibody library. The vaccine composition comprising the antibodies or antigen binding fragments against HCV B1 or E2 antigen or its hypervariable region is useful in treating or preventing HCV infection in a subject. Sequences ABG76513-ABG76568 represent human monoclonal antibodies against HCV E1 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, HCV; hepatitis C virus, El antigen; monoclonal antibody, vaccine;
hepatotropic; Fab; hypervariable region; E2 antigen; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccine comprising a human monoclonal antibody against hepatitis C virus (HCV) \rm El or \rm E2 antigen, useful for treating or preventing HCV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                              Disclosure; Page 36; 64pp; English.
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 121 AA;
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DB 5; Length 128;

100.0%; Score 29;

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The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a producter operably linked to the nucleic acid
cenceding a polypeptide whose expression is inhibited by the antisense
nucleic acid; (2) a host cell containing the vector; (3) an isolated
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
contisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
contiferation or the activity of a gene in an operon required for
proliferation or the activity of a gene in an operon required for
contisense product or that has an activity against a biological pathway
required for proliferation, or that inhibits proliferation; (8)
contisense nuclei; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the gene
compound's activity; (11) a culture comprising strains in which the gene
compound's activity; (11) a culture comprising strains in which the gene
compound activity; (11) a culture comprising strains in which the gene
compound of an organism. The antisense nucleic acids are useful for
contisting proteins or screening for homologous nucleic acids required
for cellular proliferation to isolate candidate molecules for rational
drug discovery programs, or for screening homologous nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antiBense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                     Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zyskind JW;
Xu HH;
                 Gaps
                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohlsen KL,
Forsyth RA,
                 Indels
                                                                                                                                                                                                                                                                                                     Protein encoded by Prokaryotic essential gene #10334.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; SEQ ID NO 52731; 1766pp; English.
                 Mismatches
 Pred. No.
                                                                                                                                                                                         ABU24807 standard; protein; 206 AA.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00372851.
06-MAR-2002; 2002US-0362699P.
100.04;
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                                                                                                                                                                                                                                                                    (first entry)
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                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-029926/02.
N-PSDB; ACA28677.
Best Local Similarity
Matches 5; Conserv
                                                                                            32 TYAMH 36
                                                       1 TYAMH 5
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                                                                                                                                                                                                                                                                    19-JUN-2003
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                                                                                                                                                                                                                              ABU24807;
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Wall
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The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and polynucleotides encoding them. The sequences are useful in diagnosis and polynucleotides encoding them. The sequences are useful in diagnosis and prophylaxis and treatment of pathological conditions resulting from a prophylaxis and treatment of pathological conditions resulting from a compound, such as a polypeptide, or fetcive antibacterial targets, as targets for antibacterial durgs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed produced part of the printed patent patent of the printed patent patent patent forms the patent forms forms the patent forms the patent forms forms the patent forms forms the patent forms forms the patent forms forms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                         Length 206;
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100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, SEQ ID NO 26228; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nolling J, Deloughery C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa polypeptide #9657,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABO77482 standard; protein; 258 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seqdata.uspto.gov/sequence.html
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                                                                                                                                                                                                                                                                                               5; Conservative
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                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                  30 TYAMH 34
                                                                                                                                                                                                                                                                                                                                                 1 TYAMH 5
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                                                                                                                                                                                           Sequence 206 AA;
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us-10-614-959-10.rag

Gaps ö Query Match
100.0%; Score 29; DB 7; Length 258; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 5; Conservative 0; Mismatches 0; Indels

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1 TYAMH 5

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201 TYAMH 205 셤 ADN27332 standard; protein; 278 AA

ADN27332;

02-DEC-2004 (first entry)

Bacterial polypeptide #9985

Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; heat tolerance; pathogen tolerance; pest tolerance; plant disease resistance; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

US2003233675-A1

18-DEC-2003

20-FEB-2003; 2003US-00369493

21-FEB-2002; 2002US-0360039P

CAOY/)

CAO Y.
HINKLE G J.
SLATER S C.
CHEN X.
GOLDMAN B S. (HINK/) (SLAT/) (CHEN/) (GOLD/)

Goldman BS; Chen X, Hinkle GJ, Slater SC, Cao Y,

WPI; 2004-061375/06

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polymucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Claim 1, SEQ ID NO 9985; 122pp; English.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant the case of soybean. The method of producing a plant with the recombinant DNA construct and growing the transforming a plant with the compinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for improving plants with the improved plant properties, e.g. improved cold, heat or drought tolerance, colerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modification of carbohydrate, nitrogen or content, improved yield by modification of photosynthesis or by phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lightin production or improved galactomannan RESULT 9

ADN27332

ID ADN27332

XXX ADN2

XXX ADN2

XXX Reco

XXW Reco

XXW Reco

XXW Reco

XXW Dath

XXW CAP

XX

production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at segdata.uspto.gov/sequence.html. 8888888

Sequence 278 AA;

ö Length 278; 0; Indels Query Match
100.0%; Score 29; DB 8; L
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Best Loca Matches

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Gaps

220 TYAMH 224 1 TYAMH S

ઠે 셤 RESULT 10 AAG72483

AAG72483 standard; protein; 307 AA

AAG72483;

(first entry) 31-JUL-2001

Human OR-like polypeptide query sequence, SEQ ID NO: 2164

Human, olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.

Homo sapiens

WO200127158-A2

19-APR-2001

06-OCT-2000; 2000WO-US027582.

08-OCT-1999; 99US-0158615P. 24-FEB-2000; 2000US-0184809P.

(DIGI-) DIGISCENTS. (YEDA) YEDA RES & DEV CO LTD.

Yanai Fuchs T, Lancet D, Glusman G, Smith D, Bellenson J,

WPI; 2001-290713/30

New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists.

Example 6; Page 1455-1456; 1857pp; English.

The present sequence is a polypeptide encoded by one of 144 newly mined human genes. It was used as a query sequence in a database search of olfactory receptor (OR)-like sequences. The invention relates to isolated polynucleotides encoding polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and artagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different

Sequence 307 AA;

DB 4; Length 307; 100.0%; Score 29;

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human, oligo-capping method, diagnostic marker; gene therapy; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia; short memory; cancer; sense er motor function; emocional reaction; fear response; panic; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
                                                                                     Human protein useful for treating neurological disease Seq 3799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                   .2-FEB-2004; 2004EP-00003145.
                                                                                                                                                                                                                                                                                                                                                                                                                       14-FEB-2003; 2003JP-00102207.
                                                     04-NOV-2004 (first entry)
                                                                                                                                                                                                                                tranquiliser.
                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                       EP1447413-A2
                                                                                                                                                                                                                                                                                                                                               18-AUG-2004.
                   ADR10293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              office.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining the interaction pattern of a composition with the receptors, and can be used for determining the interaction of the interaction of the interaction pattern of a composition with the receptors, and can be used for determining the interaction of th
                       Gaps
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                                                                                                                                                                                                                                                                                                                                             Human, olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yanai I;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 29; DB 4; Length 321; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fuchs T,
                                                                                                                                                                                                                                                                                                           Human olfactory receptor polypeptide, SEQ ID NO: 1156.
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   Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glusman G,
                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 674-675; 1857pp; English
                                                                                                                                                                                                AAG71475 standard; protein; 321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lancet D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-OCT-2000; 2000WO-US027582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-OCT-1999; 99US-0158615P.
24-FEB-2000; 2000US-0184809P.
   100.08;
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                 154 TYAMH 158
                                                             1 TYAMH 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                          31-JUL-2001
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                                                                                                                                                            RESULT 11
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This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to molecules and the encoded proteins thereof. Specifically, it refers to constant a constant and signal method, where none of these clones are identical to any known human mRNAs. The present invention describes an immunoassay to identify agonists and antagonists, as well as antibodies, antisense molecules and siRNAs that can all be used to bind to antibodies, antisense molecules and siRNAs that can all be used to bind to antibodies are useful for diagnostic markers or therapeutic targets for the various diseases or morbid states. In particular, they are useful in gene therapy for treating osteoporosis, neurological disease, Alzhaimer's disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or morbor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, cytostatic and tranquiliser activities. This polypeptide is a protein encoded by a full length human cDNA sequence of the invention. NOTE: This sequence is not given in the sequence listing of the specification but sequence is not proper by the property of the specification but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                     New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
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   Otsuki
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T, Isono Y, Sugiyama T, Irie R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 29; DB 8; Length 531; 100.0%; Pred. No. 3.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 3799; 2686pp; English.
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   Nishikawa
                                                Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 100.
5; Conservative
           Isogai T, Yamamoto J,
Wakamatsu A, Ishii S,
                                                                                                                    WPI; 2004-583265/57
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                                                                                                                                                      N-PSDB; ADR08337
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Best Local S
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ADR10293 standard; protein; 531 AA.

RESULT 12 ADR10293 ID ADR103

169 TYAMH 173

1 TYAMH 5

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Aspergillus oryzae-originated glutaminase and partial amino-acid sequences for enhancing taste particularly in glutamic acid-convarting food processing to make e.g. seasoning sauces and pastes.
                                                  Glutaminase, decomposition, glutamine, glutamic acid, ammonia, taste enhancer, seasoning, sauce, paste.
                                                                                                                                                                                                                                               Koibuchi K, NagaBaki H, YuaBa A, Kataoka J, Kitamoto K;
                                                                                                    1. .20
/label= signal_peptide
21. .690
                                                                                                                                                                                                                                                                                                                          Example 3; Page 52-55; 74pp; Japanese.
                                                                                            Location/Qualiflers
                                  A. oryzae glutaminase protein #2.
                                                                                                                                                                                    98JP-00134080.
98JP-00258974.
98JP-00292443.
99JP-00089157.
                                                                                                                                                                      99WO-JP002455
                 (first entry)
                                                                                                                                                                                                                               (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                                                                                                                                 WPI; 2000-053292/04.
N-PSDB; AAZ43684.
                                                                          Aspergillus oryzae.
                 24-FEB-2000
                                                                                                                                    W09960104-A1
                                                                                                                                                                     12-MAY-1999;
                                                                                                                                                                                              11-SEP-1998;
                                                                                                                                                                                     15-MAY-1998;
                                                                                                                                                    25-NOV-1999
                                                                                                                                                                                                               30-MAR-1999;
                                                                                           Key
Peptide
                                                                                                                    Protein
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This invention describes a novel glutaminase enzyme isolated from Aspergillus oryzae which catalyses the decomposition of glutamine to glutamic acid and ammonia. The purified glutaminase and determined partial amino-acid sequence can be used for enhancing taste particularly and pattes as well as other seasoning materials. The gene thus obtained can be applied as probe for hybridization providing the gene-containing DNA fragments from genome and cDNA libraries of A. oryzae and A. nidulans, and subsequently modified glutaminase-producing breed. The secreting ability. This sequence represents the A. oryzae glutaminase enzyme described in the method of the invention

Sequence 690 AA;

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Gapa
                                               ö
   100.0%; Score 29; DB 3; Length 690; 100.0%; Pred. No. 4.5e+02; Live 0; Mismatches 0; Indels
Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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AAY50835 standard; protein; 690 AA AAY50835; RESULT 14 AAY50835 ID AAY5 XX AC AAY5 XX DT 24-F XX DE A. ¢

24-FEB-2000 (first entry)

A. oryzae glutaminase protein #1.

This invention describes a novel glutaminase enzyme isolated from Aspergillus oryzae which catalyses the decomposition of glutamine to glutamic acid and ammonia. The purified glutamines and determined partial amino-acid sequence can be used for enhancing taste particularly in glutamic acid-converting food processing to give e.g. seasoning sauces and pastes as well as other seasoning materials. The gene thus obtained can be applied as probe for hybridization providing the gene-containing DNA fragments from genome and cDNA libraries of A. oryzae and A. nidulans, and subsequently modified glutaminase-producing breed. The novel strain of A. oryzae is a highly active because of its somatic secreting ability. This sequence represents the A. oryzae glutaminase enzyme described in the method of the invention Aspergillus oryzae-originated glutaminase and partial amino-acid sequences for enhancing taste particularly in glutamic acid-converting food processing to make e.g. seasoning sauces and pastes. Glutaminase; decomposition; glutamine; glutamic acid; ammonia; taste enhancer; seasoning; sauce; paste. Kitamoto K; Koibuchi K, Nagasaki H, Yuasa A, Kataoka J, 1. .20 /label= signal_peptide 21. .690 Claim la; Page 41-44; 74pp; Japanese. Location/Qualifiers 98JP-00134080. 98JP-00258974. 98JP-00292443. 99JP-00089157. 99WO-JP002455 (AJIN) AJINOMOTO CO INC. WPI; 2000-053292/04. N-PSDB; AAZ43677. oryzae Sequence 690 AA; 15-MAY-1998; 11-SEP-1998; 14-OCT-1998; WO9960104-A1 12-MAY-1999; Aspergillus 30-MAR-1999; 25-NOV-1999. Protein Peptide

ö Gapa ö Ouery Match
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels ઠે

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Aspergillus oryzae KBN616 glutaminase. AAB14781 standard; protein; 703 AA. 06-DEC-2000 (first entry) AAB14781;

Glutaminase; Aspergillus oryzae KBN616; glutamic acid synthesis; fermentation; foodstuff production; miso; soy sauce.

Aspergillus oryzae

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This sequence represents a novel glutaminase from Aspergillus oryzae KBN616. The invention relates to two novel glutaminases (AAB14781, AAB14782) from Aspergillus oryzae KBN616 and Aspergillus sojae BA-104 respectively which have molecular weights of approximately 73 kD (as determined by gel filtration). The enzymes have an optimum temperature of approximately 50 degrees Celsius, and an optimum ph of about 8.5. The glutaminases catalyse the conversion of L-glutamine to L-glutamic acid, and may be used in the production of fermented foodstuffs such as soy
             Location/Qualifiers
34. .703
/note= "Mature glutaminase; specifically claimed"
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100.0%; Score 29; DB 3; Length 703;

Best Local Similarity 100.0%; Pred. No. 4.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                    A new glutaminase and its preparation.
                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 15-17; 27pp; Japanese.
                                                                                                                                         98JP-00347127.
                                                                                                                                                                         98JP-00347127.
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N-PSDB; AAA72204.
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERSINCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
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Best Local Similarity 100.0%; Pred. No. 1.18+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: PCT/JP99/02455
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 690
TYPE: PRT
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US-10-262-083-18
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GENERAL INFORMATION:

APPLICANT: KOIBUCHI, Kyoko

APPLICANT: YUASA, Ari

APPLICANT: YUASA, Ari

APPLICANT: KITAMOTO, Katsuhiko

APPLICANT: KITAMOTO, Katsuhiko

APPLICANT: KITAMOTO, Katsuhiko

TITLE OF INVENTION: A No. 6830905e1 Glutaminase, its Gene and a Method of Producing I

FILE REFERENCE: 19943905-822-10-0-PCT

CURRENT APPLICATION NUMBER: US/10/262,083

CURRENT FILING DATE: 2000-11-15

PRIOR APPLICATION NUMBER: UP 10/134080

PRIOR FILING DATE: 1998-09-11

PRIOR PILING DATE: 1998-09-11

PRIOR PILING DATE: 1998-10-14

PRIOR APPLICATION NUMBER: UP 10/258974

PRIOR PILING DATE: 1998-10-14

PRIOR APPLICATION NUMBER: JP 10/292443

PRIOR PILING DATE: 1998-10-14

PRIOR PILING DATE: 1999-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

Agglance 26228, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

AFPLICATION:

AFPLICATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

TITLE OF INVENTION:

ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE:

PRIOR PELICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 258
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100.0%; Score 29; DB 4; Length 258;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels
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Patent No. 6830905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26228
                    ; EARLIER FILING DATE: 1996-05-23
; NUMBER OF SEQ ID NOS: 60
; SCOTWARE: Patentin Ver. 2.0
; SEQ ID NO 45
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Murine
US-09-232-290-45
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152 TYALH 156

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US-09-543-681A-8288

Sequence 8288, Application US/09543681A

Sequence 8288, Application US/09543681A

Sequence 8288, Application US/09543681A

Sequence 8288, Application US/09543681A

SETILE NET CANY GARY BRETON

TITLE OF INVENTION: UDLESC AND THERAPEUTICS

FILE REFRENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT APPLICATION NUMBER: US/09/543,681A

SEQ ID NO 8288

SEQ ID NO 8288

LENGTH: 455

TYPE: PRT

ORGANISM: Proteus mirabilis

US-09-543-681A-8288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5992, Application US/09949016

| Sequence 5992, Application US/09949016
| Patent No. 681239
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| CURRENT APPLICATION NUMBER: US/09/949,016 |
| PRIOR APPLICATION NUMBER: 60/241,755 |
| PRIOR FILING DATE: 2000-10-20 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-03 |
| NUMBER OF SEQ ID NOS: 207012 |
| SOFTWARE: PSESEE for Windows Version 4.0 |
| LENGTH: 502 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 455;
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Sequence 7091, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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Pred. No. 3.6e+02;
1; Mismatches 0;
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80.0%; Pred. No. 3.9e+02;
iive 1; Mismatches 0.
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0°
Local 4; Conservative
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225 TYALH 229
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US-09-949-016-5992
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ORGANISM: 1
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Patent No. 6610830
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 10284
LENGTH: 454
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US-09-270-767-50714
Sequence 50714, Application US/09270767
Factor No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 50714
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Pred. No. 85;
1; Mismatches 0; Indels
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80.0%; Pred. No. 85;
tive 1; Mismatches
                                                                                                                            ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-35497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-50714
                                                                                  ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Klebsiella pneumoniae
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 35497
LENGTH: 108
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0°
Matches 4; Conservative
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64 TYALH 68
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64 TYALH 68
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US-09-489-039A-10284
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Pred. No. 4.3e+02;
1; Mismatches 0; Indels
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MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS-DOS 6.00 SOFTWARE: ASCII Editor CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APFILING DATE:
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 362-0823
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                            ); NAME/KEY; misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 4113161CD1
US-09-919-039-270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOGY: linear
                                                                                                                                                                                            89.78;
                                                                                                                                                                                          Query Match
Best Local Similarity 80.0
Matches 4; Conservative
        SEQ ID NO 270
LENGTH: 544
TYPE: PRT
ORANISM: Homo sapiens
FEATURE:
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Matches 4; Conserv
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US-08-918-148-26
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US-08-264-093-21
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; Sequence 699, Application US/09976594
; Patent No. 6673549
; General Incomation; General Sequence 699, Application US/09976594
; GENERAL INFORMATION:
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2000-10-12
; VERNOR PILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL PROGram
; SEQ ID NO 699
; LANGTH: 544
; TYPE: PRT

TYPE: PRT

TYPE: PRT

GRANISM: Homo sapiens
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR PRDILGATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
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Pred. No. 4e+02;
1; Mismatches 0; Indels
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// OTHER INFORMATION: Incyte ID No. 6673549 4113161CD1
US-09-976-594-699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

89.7%; Score 26; DB 4; 1
Best Local Similarity 80.0%; Pred..No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0;
              CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 7091
LENGTH: 507
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                                                                                                                                                                                                                                                                                                                                                          89.7%;
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Best Local Similarity 80.0
Matches 4; Conservative
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485 TYALH 489
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                                                                                                                                                                                                                                                                                                 , ORGANISM: Human
US-09-949-016-7091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-09-976-594-699
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Page 5
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us-10-614-959-10.rai
                                                                           Sequence 26, Application US/08918148A

Patent No. 6342220
GENERAL INFORMATION:
APPLICANT: Adams, Camellia
APPLICANT: W.
APPLICANT: Garter, Paul J.
APPLICANT: Garter, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: 10979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 26
LENGTH: S
TYPE: PRT
ORGANISM: artificial
FRATURE:
NAMEKEY: 10D108cFv, 12B5scFv VH CDR1
COCATION: 1-5
COTHER INFORMATION:
US-08-918-148-26
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Search completed: October 14, 2005, 16:22:00 Job time : 10.8438 secs

1 TYAMH 5 || || 1 TYGMH 5

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Query Match 86.2%; Score 25; DB 3; Length 5; Best Local Similarity 80.0%; Pred. No. 4.1e+05; Matches 4; Conservative 0; Mismatches 1; Indels

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us-10-614-959-10.rapb

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

October 14, 2005, 16:20:10; Search time 35:5469 Seconds (without alignments) 58.615 Million cell updates/sec Published Applications AA:*

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5: /cgn2_6/ptodata/2/pubpaa/US08_NEM_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
7/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:* Total number of hits satisfying chosen parameters: 1859788 seqs, 416717961 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Minimum DB seq length: 0 Maximum DB seq length: 200000000 US-10-614-959-10 29 1 TYAMH 5 Title: Perfect score: Sequence: Database : Searched: Run on:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		Sequence 91, Appl	12.	25	,	Sequence 47, Appl	31	Sequence 231272.	Sequence 211694.	Sequence 52731. A	Sequence 34. Appl
ŪΙ	US-10-989-462-64	US-10-468-543-91	US-11-003-819-12	US-10-466-242-25	US-10-989-462-7	US-10-466-242-47	US-10-425-115-311733	US-10-424-599-231272	US-10-425-115-211694	US-10-282-122A-52731	US-10-989-462-34
рв	18		20	16	18	16	16	15		15	
Query Match Length DB ID	.5	11	119	121	123	128	137	151	158	206	257
Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	29	29	29	29	29	29	29	29	29	29	29
Result No.	н	7	m	4	S	9	7	ω	đ	10	11

Sequence 9985, Ap Sequence 2, Appli Sequence 18, Appl		Sequence 254835, Sequence 188939,	Sequence 363604,	edneuc	Sequence 109084,	Sequence 2485/4,	Sequence 190876,		Seguence 192746,		245		e 193	485	214					2980,		205	455	42,	3768	\$17
US-10-3 US-10-2 US-10-2	US-10-468-543-	US-10-425-115-2 US-10-425-115-1	US-10-425-115-3	US-10-424-599-18825	US-10-437-963-1	-	US-10-424-599-1	US-10-425-115-27191	424-599-19274	424-599-2	3-10-424-599-24558	2	US-10-091-483-193	-48	٢	٦	٩	7	-3998	US-10-094-749-2980	?	۲	US-10-282-122A-45565	S-10-831	-09-738-626-	US-09-738-626-5177
14 14 15	16	16	16	12	16	9 0	15	16	15	15	15	σ	14	16	15	16		15					15		σ	σ
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1111 1111 1111	16	18 13	20	22	23	2 2	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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US-10-999-462-64

Sequence 64, Application US/10989462

Publication No. US20050220795A1

GENERAL INFORMATION:
APPLICANT: Wittrup, K. Dane
APPLICANT: Wittrup, K. Dane
TITLE OF INVENTION: ANTI-HYDROXYLASE ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 01997-329001
CURRENT APPLICATION NUMBER: US/10/989,462
CURRENT PILING DATE: 2004-11-15
FRIOR APPLICATION NUMBER: US 60/520,114
FRIOR APPLICATION NUMBER: US 60/520,114
FRIOR PRILING DATE: 2003-11-14
FRIOR PILING DATE: 2004-04-19
SOFTWARE: FRAUESQ FOR WINDOWS VERSION 4.0

SEQ ID NOS: 319
SEQ ID NOS: 319
SEQ ID NOS: 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Synthetically generated peptide US-10-989-462-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 29; DB 18;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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APPLICANT: Persson, Mats
TITLE OF INVENTION: Materials and methods for treatment of hepatitis C
FILE REFERENCE: 0380-9032480S00
CURRENT APPLICATION: MUMBER: US/10/466,242
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: PCT/SE02/00044
PRIOR PILING DATE: 2002-01-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 29, DB 16; Length 121;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-98-462-7

Sequence 7, Application US/10989462

Sequence 7, Application US/10989462

Publication No. US20050220795A1

GENERAL INPORMATION:

APPLICANT: Wittrup, K. Dane

APPLICANT: Wittrup, Xi Andy

ITLE OF INVENTION: ATHT-HYDROXYLASE ANTIBODIES AND USES

ITLE OF INVENTION: THEREOF

FILE REFERENCE: 01997-329001

CURRENT APPLICATION NUMBER: US/10/989,462

CURRENT APPLICATION NUMBER: US/06/520,114

PRIOR FILING DATE: 2004-11-15

PRIOR FILING DATE: 2004-11-14

PRIOR FILING DATE: 2004-01-19

NUMBER OF SEQ ID NOS: 319

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 123
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, OTHER INFORMATION: Synthetically generated peptide
US-10-989-462-7
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Sequence 47, Application US/10466242

Publication No. US2004020887A1

PENERAL INFORMATION:

APPLICANT: Drakenberg, Katarina
Sequence 25, Application US/10466242
Publication No. US20040208887A1
GENERAL INFORMATION:
APPLICANT: Drakenberg, Katarina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: PEPTIDE
; LOCATION: (1)..(121)
; OTHER INFORMATION: Clone 2a:14 VH
US-10-466-242-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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                                                               Sequence 91. Application US/10468543
; Sequence 91. Application US/10468543
; Publication No. US20040091938A1
; GENERAL INFORMATION:
; APPLICANT: Irimura, Tatsuro
; APPLICANT: Matsumoto, Mariko
; APPLICANT: Yim, Mijuug
; APPLICANT: Yim, Mijuug
; APPLICANT: Ono, Takeshi
; TITLE OF INVENTION: Lectins for Analyzing Sugar Chains and Method of Using the Same
; FILE REFERENCE: 03-786
; CURRENT APPLICATION NUMBER: US/10/468,543
; CURRENT FILING DATE: 2001-02-20
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 91
; TANOTH: 11
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Squence 12, Application US/11003819

Publication No. US2005015832341

GENERAL INFORMATION:

APPLICANT: Evans, Elizabeth E.

APPLICANT: Sahasrabudhe, Deepak M.

APPLICANT: Sahasrabudhe, Deepak M.

APPLICANT: Salasrabudhe, Deepak M.

APPLICANT: Salasrabudhe, Deepak M.

APPLICANT: Salasrabudhe, Deepak M.

TITLE OF INVENTION: Methods of Killing Tumor Cells by Targeting Internal Antigens

TITLE OF INVENTION: Methods of Killing Tumor Cells

TITLE OF INVENTION: Methods of Killing Tumor Cells

TITLE OF INVENTION: Methods of Killing Tumor Cells

TITLE OF INVENTION: WOMBER: US/11/003,819

CURRENT APPLICATION NUMBER: US 60/256,572

PRIOR FILING DATE: 2003-12-04

PRIOR PELING DATE: 2003-12-23

NUMBER OF SEQ ID NOS: 61

SOFTWARE: Patentin version 3.3

SEQ ID NO 12

LENGTH: 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 29; DB 15; Length 11; Best Local Similarity 100.0%; Pred. No. 7.2; Matches 5; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 5, Conservative
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CRGANISM: Homo sapiens
US-11-003-819-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial
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US-10-466-242-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-468-543-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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Gaps

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PEATURE:
NAME/KEX: unsure
(1)..(158)
OTHER INFORMATION: unsure at all xaa locations
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Sequence 52731, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 211694, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION:
             CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ 1D NOS: 285684 ESQ 1D NO 231272 LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TYAMH 5
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Sequence 311733, Application US/10425115

PUBLICATION: US.0040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Acoalic, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: 130-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 311733

LENGTH: 137
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
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APPLICANT: Persson, Mats
TITLE OF INVENTION: Materials and methods for treatment of hepatitis C
FILE REPERSIVE: 0180-0902480800
CURRENT PILING DATE: 2004-01-16
PRIOR TILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: PCT/SE02/00044
PRIOR PILING DATE: 2002-01-14
SEQ ID NOS: 56
SOFTWARE: Patentin version 3.1
LENGTH: 128
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity 100.0%; Score 29; DB 16; Length 128;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: PEPTIDE
; COCATION: (1)..(128)
; OTHER INFORMATION: Clone 2b:5 VH
US-10-466-242-47
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||||
16 TYAMH 20
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                                                                                                                                                                                                                                                                                                                                               FEATURE:
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thua
APPLICANT: Cao, Yinua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)8
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 211694
LENGTH: 158
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                                                                                                                                                                                                                                                                 100.0%; Score 29; DB 15; Length 151; 100.0%; Pred. No. 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 29; DB 16; Length 158; 100.0%; Pred. No. 94; tive 0; Mismatches 0; Indels (
TYPE: RT
ORGANISM: Glycine max
ORGANISM: Glycine max
FEATURE:
NAME:
COCATION: (1). (151)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
COTHER INFORMATION: Clone ID: PAT_MRT3847_50860C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Clone ID: MRT4577_124664C.1.pep US-10-425-115-211694
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Matches
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                                                                     APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034
FULE REPERENCE: ELITRA.034
FULE REPERENCE: ELITRA.034
PRIOR APPLICATION NUMBER: 05/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PLLING DATE: 2000-03-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-05-06
PRIOR PLLING DATE: 2000-05-06
PRIOR PLLING DATE: 2000-05-06
PRIOR PPLICATION NUMBER: 60/230,347
PRIOR PPLICATION NUMBER: 60/230,347
PRIOR PPLICATION NUMBER: 60/230,347
PRIOR PPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/25,578
PRIOR APPLICATION NUMBER: 60/25,658
PRIOR APPLICATION NUMBER: 60/257,636
PRIOR PPLING DATE: 2000-10-22
PRIOR APPLICATION NUMBER: 60/257,636
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/259,308
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| Publication No. US20050220795A1
| GENERAL INFORMATION:
| APPLICANT: Withturp, K. Dane
| APPLICANT: Yeung, Yik Andy
| TITLE OF INVENTION: ANTI-HYDROXYLASE ANTIBODIES AND USES
| TITLE OF INVENTION: THEREOF
| FILE REFERENCE: 01997-329001
| CURRENT APPLICATION NUMBER: US/10/989,462
| CURRENT APPLICATION NUMBER: US 60/520,114
| PRIOR FILING DATE: 2004-11-15
| PRIOR FILING DATE: 2004-10-16
| PRIOR FILING DATE: 2004-04-19
| NUMBER OF SEQ ID NOS: 319
| SOFTHARE: PRESENCE: 2004-04-19
| SOFTHARE: PRESENCE: ANTIBODIES AND USES
| SOFTHARE: PRIOR FILING DATE: 2004-04-19
| SOFTHARE: PRESENCE: 2004-04-19
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US-10-989-462-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 29; DB 18; 100.0%; Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Clostridium botulinum US-10-282-122A-52731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Seguence
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
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US-10-262-U83-2

Sequence 2, Application US/10262083

Sequence 2, Application US/10262083

Fublication No. US20030170670A1

GENERAL INFORMATION:
APPLICANT: KOIBUCHI, Kyoko
APPLICANT: KURAKA, Ari
APPLICANT: KATAKOKA, Jiro
APPLICANT: KATAKOTO, Kateuhiko
TITLE OF INVENTION: A No. US20030170670Alel Glutaminase, its Gene and a Method of Proc
TITLE OF INVENTION: A No. US20030170670Alel
FILE REFRENCE: 19943805-822-10-0-22
CURRENT PRILING DATE: 2000-11-15
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-09-11
PRIOR FILING DATE: 1999-03-10
PRIOR PLING DATE: 1999-03-10
                                                                                                                                                                                                                                         US-10-369-493-9985

US-10-369-493-9985

Publication US/10369493

Publication No. US20030233675A1

Publication No. US20030233675A1

APPLICANT: Cao, Yongwei

APPLICANT: APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10 (52052)B

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 9985

LENTH: 278
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; ORGANISM: magnetite-containing magnetic coccus
US-10-369-493-9985
       Mismatches
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           5, Conservative
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31 TYAMH 35
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Query Match 100.0%; Score 29; DB 16; Length 690; Best Local Similarity 100.0%; Pred. No. 3.9e+02; Matches 5; Conservative 0; Mismatches 0; Indels
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: JP 10/258974
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR PILING DATE: 1998-10-14
PRIOR PILING DATE: 1998-10-14
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-05-12
PRIOR FILING DATE: 1999-05-12
PRIOR APPLICATION NUMBER: PCT/JP99/02455
PRIOR FILING DATE: 1999-05-12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
SLENGTH: 690
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                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-851-337-2
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Sequence 18, Application US/10262083

Sequence 18, Application US/10262083

Sequence 18, Application No. US20030170670A1

GENERAL INFORMATION:

APPLICANT: WIGABAKI, Hiroaki

APPLICANT: WIGABKI, AN: US20030170670A1e1 Glutaminase, its Gene and a Method of Pro

CURRENT APPLICANTON NUMBER: US/10/262,083

PRIOR APPLICANTON NUMBER: US/99/674,507

PRIOR APPLICANTON NUMBER: UP 10/134080

PRIOR FILING DATE: 1998-09-11

PRIOR FILING DATE: 1998-09-11

PRIOR FILING DATE: 1998-10-14

PRIOR FILING DATE: 1999-10-30

SOCTWARE: PAPELICANTON NUMBER: PCT/JP99/02455

NUMBER OF SCO ID NOS: 26

LENGTH SCOT DATE: 1999-10-30

TWOE: DATE

LENGTH: 690
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Sequence 2, Application US/10851337

Publication No. US2004022932A1

GENERAL INFORMATION:

APPLICANT: NAGASAKI, Hiroaki

APPLICANT: NAGASAKI, Hiroaki

APPLICANT: KATAOKA, Jiro

APPLICANT: KATAOKA, Jiro

APPLICANT: KATAOKA, Jiro

APPLICANT: KITAMOTO, Katsuhiko

ITILE OF INVENTION: Producing It

FILE REFERENCE: 199438US-8222-10-0-PCT

CURRENT APPLICATION NUMBER: US/10/851,337

CURRENT FILING DATE: 2004-05-24

PRIOR APPLICATION NUMBER: US/10/262,083

PRIOR PAPLICATION NUMBER: US/10/10-15

PRIOR APPLICATION NUMBER: US/10/10-15
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                                       Length 690;
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                              Query Match
100.0%; Score 29; DB 14; Length 6.
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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Сарв

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

October 14, 2005, 16:02:59; Search time 6.95312 Seconds (without alignments) 69.190 Million cell updates/sec Run on:

US-10-614-959-10 29 Title: Perfect score:

1 TYAMH S

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Iq heavy chain V-I	heavy chain	e kinas		hypothetical prote	ι'	hypothetical prote	•	hypothetical profe	conserved hypothet	hypothetical prote	B. subtilia von n	Bubt 1118	tochrome P450 3	P450	P450	P450	al pro		æ	pol polyprotein -	pol polyprotein -	pol protein - bovi	fix23-3 protein -	probable helicase	hypothetical prote	>	polyketide synthas	Ig heavy chain V r
SUMMARIES		a ib			2 D71184	2 B83290					: H86403			: AD1165	2 AD1524		. A34236	A34101			-		GNLJGA	GNLJGB		S18955		T21706	T30886		
		Length DB	122					1377	95											609				852 1			265	385		260	
٠	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	σ	σ	σ	g	6	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	ę.	ď.	<u>ه</u> .	89.7	ģ	89.7	89.7	89.7	86.2
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Ig heavy chain v r	leavy
846473 PLO120 S17609 S17609 S10385 S26885 S25886 S25886 S25546 S25546 S53076 PH1665 PH1665 PH1645 EN1644 EN1644 EN1645 EN1644	
24 20 20 20 20 20 20 20 20 20 20 20 20 20	
0.000000000000000000000000000000000000	10
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	25
	45

ALIGNMENTS

RESULT 1	Ig heavy chain V-III region (Ga) - human (tentative sequence) C;Species: Homo sapiens (man)	C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004 C;Accession: A02052	R;Florent, G.; Lehman, D.; Putnam, F.W. Biochemistry 13, 2482-2498, 1974	A;Title: The switch point in mu heavy chains of human IgM immunoglobulins. A;Reference number: A02052; MUID:74175307; PMID:4208843	A:Accession: A02052	A.Residues: 1-122 <flo></flo>	A;Cross-references: UNIPROT:P01769	C; Comment: This chain was isolated from a Waldenstrom's macroglobulin.	A;Gene: GDB:IGHV@	A;Cross-references: GDB:128528; OMIM:147070	A, Map position: 14q32.33-14q32.33	C; Superfamily: immunoglobulin V region; immunoglobulin homology	C: Keywords: heterotetramer; immunoglobulin; pyroglutamic acid	File-Sel Jonain: Immunoglobulin homology < IMM >	7,770cilled site: Pylrolldone Carboxyllc acid (Gin) #status experimental F;22-96/bisulfide bonds: #status predicted	
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Gарв ö Query Match 100.0%; Score 29; DB 1; Length 122; Best Local Similarity 100.0%; Pred. No. 8; Matches 5; Conservative 0; Mismatches 0; Indels

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RESULT 2
A35676
Ig heavy chain precursor V-D-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 23-Jul-1999
C;Accession: A35676
R;White, M.B.; Word, C.J.; Humpries, C.G.; Blattner, F.R.; Tucker, P.W.
Mol. Cell. Biol. 10, 3690-3689, 1990
A;Title: Immunoglobulin D switching can occur through homologous recombination in human & A;Title: Immunoglobulin D switching can occur through homologous recombination A35676
A;Accession: A35676; MUID:90287160; PMID:2113175
A;Accession: A35676
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-138 cWHIN
A;Coss-references: GB:M38066; NID:g185466; PIDN:AAA52974.1; PID:g553407
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology < IMM>

||||| 50 TYAMH 54

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1 TYAMH 5

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hypothetical protein ZK1248.17 - Caenorhabditis elegans
hypothetical protein ZK1248.17 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T34500
B;Latrellle, P.
Submitted to the EMBL Data Library, June 1995
A;Pescription: The sequence of C. elegans cosmid ZK1248.
A;Resicuence number: Z21534
A;Recession: T34500
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-95 klAT
A;Residues: 1-95 klAT
A;Residues: 1-95 klAT
A;Experimental source: strain Bristol N2; clone ZK1248
C;Genetics:
A;Genetics:
A;Genetics:
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: 154632
P;Provence, D.L.; Curtiss, R.
Infect. Immun. 62, 1369-1380, 1994
A;Title: Isolation and characterization of a gene involved in hemagglutination by an avit
A;Reference number: 154632
A;Recession: 154632
A;Accession: 154632
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1377 <RES>
A;Residues: 1-1377 <RES>
A;Coss references: UNIPROT: Q47692; GB:L27423; NID:g469235; PIDN:AAA24698.1; PID:g469236
C;Superfamily: IgA-specific metalloendopeptidase
                                                                                                                                            Ciracession: H7137
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinrson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDorren, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDorren, J.; Meldman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Ricession: H7134
A;Recession: H7134
A;Recession: H7134
A;Recession: H7134
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Rolecule 'Ype: DNA
A;Residues: 1-151 <COL>
A;Coss-references: UNIPROT:O83273; GB:AE001206; GB:AE000520; NID:g3322514; PIDN:AAC65235
A;Coss-references: uniprociete hypothetical protein TP0245
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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hypothetical protein TP0245 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
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100.0%; Score 29; DB 2; Length 1377;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indele C
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Date: 15-Sep-2000
R;Stover, CK.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patholy. A;Reference number: A62950; MUD:20437337; PMID:10984043
A;Recession: B83230
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <STO, MUD:20437311; GB.ARDOAD91: NID:G9948927; PIDN:AAG0623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       denylate kinase (EC 2.7.4.3) PH1753 [similarity] - Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Dyrococcus horikoshii C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004 C;Accession: D71184 Fixwarabayasi, Y:; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin M.; Ohiuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DN, Res. 5. 55-76, 1998 Fix. 55-76, 1998 Fixwarabayasi, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DN, Trile: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A71000; MUID:98344137; PMID:9679194 A;Scatus: Preliminary, nucleic acid sequence not shown; translation not shown A;Residues: 1-196 <KAW>
A;Residues: 1-196 <KAW
A;
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A, Experimental source: strain PA01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
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                                                                   Query Match 100.0%; Score 29; DB 2; Length 138; Best Local Similarity 100.0%; Pred. No. 9; Matches 5; Conservative 0; Mismatches 0; Indels
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C,Genetics: A,Gene: PH1753 C;Keywords: phosphotransferase

157 TYAMH 161

8

1 TYAMH 5

Query Match 100. Best Local Similarity 100. Matches 5; Conservative

192 TYAMH 196

RESULT 5 H71347

1 TYAMH 5

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                                                                     Query Match
Best Local Similarity 80.0%; Pred. No. 32;
Matches 4; Conservative 1; Mismatches 0; Indels
A;Map position: 2
C;Superfamily: Caenorhabditis elegans major sperm protein
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||:|| 12 TYSMH 16 1 TYAMH 5 ઠે g

retinol-binding protein precursor - chicken
C;Species: Gallus gallus (chicken)
C;Species: 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 150675; 842887
R;Vieira, A.V.; Kuchler, K.; Schneider, W.J.
NNA Call Biol. 14, 403-410, 1995
NNA Call Biol. 14, 403-410, 1995
A;Title: Retinol in avian cogenesis: molecular properties of the carrier protein.
A;Reference number: 150675; MUID:95267350; PMID:7748490

A;Accession: ISO675
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Reaidues: 1-196 <VIE>
A;Reaidues: 1-196 <VIE>
A;Cross-references: UNIPROT:P41263; EMBL:X77960; NID:G457778; PIDN:CAA54922.1; PID:G4577 C; Genetics:

C,Superfamily: lipocalin; lipocalin homology F;1-21/Domain: signal sequence #status predicted <SIG> F;36-195/Domain: lipocalin homology <LIP> F;25-181,91-195,141-150/Disulfide bonds: #status predicted

Gaps ö 89.7%; Score 26; DB 2; Length 196; 80.0%; Pred. No. 67; tive 1; Mismatches 0; Indels Ouery Match Best Local Similarity 80.0.

134 TYALH 138 1 TYAMH 5 g

hypothetical protein F28L5.12 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

Chacces of the sequence revision of the search of the search of the sequence of the sequence revision with the sequence of the

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-213 <STO>

A;Cross-references: UNIPROT:Q9C6N1; GB:AE005172; NID:g10998924; PIDN:AAG26064.1; GSPDB:Q C;Genetics: A; Map position: 1

ö Gaps ö Query Match 89.7%; Score 26; DB 2; Length 213; Best Local Similarity 80.0%; Pred. No. 73; Matches 4; Conservative 1; Mismatches 0; Indels

|||:| 202 TYALH 206

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Conserved hypothetical protein (imported) - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Accession: B90215
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-young, II.; Diffrites, A.C.; Nozera, C.J.; Medhna, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: E90215
A;Accession: E90215
A;Returus preliminary
A;Molecule type: DNA
A;Residues: 1-222 <KUR>
A;Residues: 1-222 <KUR>
A;Residues: 1-222 <KUR>
A;Generica:
A;Generi

0; Gaps 2; Length 222 0; Indels Query Match

89.7%; Score 26; DB
Best Local Similarity 80.0%; Pred. No. 76;
Matches 4; Conservative 1; Mismatches

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|||:| 14 TYALH 18 1 TYAMH 5

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hypothetical protein F58E6.8 - Caenorhabditis elegans
C;Species: Cat-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T2294
A;Reference number: Z19638
A;Reference number: Z19638
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Rocession: T2294
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Redues: 1-228 - WILA;Respecimental source: UNPROT: Q20984; EMBL: Z70754; PIDN: CAA94778.1; GSPDB: GN00023; CESP: F56
A;Experimental source: clone F58E6

C;Genetics: A;Gene: CESP:F58E6.8 A;Map position: 5

C, Superfamily: Caenorhabditis elegans hypothetical protein Y75B12A.2

/ Match 89.7%; Score 26; DB 2; Length 228; Local Similarity 80.0%; Pred. No. 78; onservative 1; Mismatches 0; Indels Query Match

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|||:| 177 TYALH 181 1 TYAMH 5

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B. subtilis YupB protein homolog lmo0724 [imported] - Listeria monocytogenes (strain EGD-C; Species: Listeria monocytogenes (c; Species: Listeria monocytogenes (c; Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 (c; Accession: AD146 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 (c; Baccession: AD146 #sequence_revision 27-Nov-2001 #sequence_revision 27-Nov-2001 #sequence_revision #sequence_

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396 TYALH 400
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      C; Genetics
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C.Species: Discription of the control of the c
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Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Varquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUD:21537279; PMID:11679669

A;Referus: preliminary

A;Molecule type: DNA

A;Residues: 1-24z <GLA>

A;Coss-references: UNIPROT:08X918; GB:NC_003210; PIDN:CAC98802.1; PID:g16410113; GSPDB:A;Everimental Bource: strain EGD-e

A;Everimental Bource: strain EGD-e

A;Genetics

A;Genetic
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C_j Superfamily: Bacillus subtilis hypothetical protein yvpB
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89.7%; Score 26; DB 2;
Best Local Similarity 80.0%; Pred. No. 83;
Matches 4; Conservative 1; Mismatches
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191 TYSMH 195
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Oylochrome P450 3A6 (version 1) - rabbit
NyAlternate names: cytochrome P450 3c
NyContains: axidoracductase (EC 1.-..)
NyContains: axidoracductase (EC 1.-..)
Cybecies: Oryctolagus cuniculus (domestic rabbit)
Cybate: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
Cybate: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
Cybate: 31-Dec-1988
NyDalet, C: Clair, P.; Daujat, M.; Fort, P.; Blanchard, J.M.; Maurel, P.
DNA 7, 39-46, 1988
A;Title: Complete sequence of cytochrome P450 3c cDNA and presence of two mRNA species way Reference number: A29487; MUID:88166352; PMID:3349903
A;Reference number: A29487
A;Residues: 1-501 cDN AA31430.1; PID:9165574
A;Residues: 1-501 cDN AA31430.1; PID:9165574

RESULT 14

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Ajdemia CYPPAS, cytochrome P450 CYPPAS, cytochrome P450 homology cytoch
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October 14, 2005, 15:51:44 ; Search time 33.2812 Seconds (without alignments) 76.932 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                  OM protein - protein search, using sw model
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US-10-614-959-10 29 1 TYAMH 5 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 Total number of hits satisfying chosen parameters:

1612378 segs, 512079187 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* **Database**:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	1 29 100.0 72 2 QBRZ81 Q8rz81 Oryza sati
	E C	72 2 QBRZ81
	8	~
	Length	72
Query	Match	29 100.0
	No. Score Match Length DB ID	29
Result	No.	-

SUMMARIES

	Description	O8rz81 orvza sativ	homod		O59443 pyrococcus	9		homod	homo	esche	-				Q9j513 fowlpox vir		O88093 escherichia				Q23428 caenorhabdi		_				Q61mv3 photobacter		_	Q9ckq5 pasteurella	-	_	
		Q8RZ81	HV3H HUMAN	Q8PKV7	KADA PYRHO	09HZ <u>Z</u> 6	Q962C9	Q6N097	Q68CN4	Q83WR9	Q6AQ19	Q9V6J4	Q9HGS1	6XVV60	V222 FOWPV	Y245_TREPA	088093	047692	Q6JHN6	Q62XJ3	023428	Q6XNP8	Q8ZZAS	Q7Z447	Q66BK2	Q86SK1	Q6LMV3	Q67RRB	RETB_CHICK	Q9CKQ5	Q9C6N1	Q9DG60	
	DB		н	~	н	~	7	~	~	~	7	~	~	~	-	н	~	~	N	~	~	~	~	~	~	~	~	~	-	~	~	~	
	Query Match Length	72	122	158	.196	249	356	481	493	531	544	648	069	069	747	1151	1377	1377	8	65	95	108	സ	160	vo	~	175	187	σ	0	213	217	
A P	Query Match	100.0	100.0	100.0	•	٠	100.0	100.0	100.0	100.0	100.0	٠	100.0	100.0	100.0	100.0	100.0	100.0	100.0	σ	89.7	σ	σ,	σ,	89.7	on .	σ	σ	o	89.7	89.7	89.7	
	Score	29	29	29	29	29	29	29	29	29	. 29	29	29	29	29	29	29	29	59	26	26	56	56	26	26	56	56	56	56	56	56	56	
	kesult No.	7	7	m	4	Ŋ	9	7	Φ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	56	27	28	59	30	31	

Q9ux67 sulfolobus	Q20984 caenorhabdi	O88hp4 trichoderma		O92dto listeria in	0722h3 listeria mo		-			bacillus	_	bacillus	
Q9UX67	Q20984	Q8SHP4	Q8Y918	Q92DT0	Q722H3	Q8WRC3	Q885R2	Q708W1	970JU6	Q65M55	063515	Q731K1	Q818Z0
7	~	~	N	~	~	N	~	~	7	7	7	~	01
222	228	229	242	242	242	244	248	266	296	302	304	304	304
89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7
26	56	56	56	56	56	56	56	56	56	56	26	56	56
32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

ULT 1 281	QBRZ81 PRELIMINARY; PRT; 72 AA. OBRZ81;	01-JUN-2002 (TrEMBLrel, 21, Created) 01-JUN-2002 (TrEMBLrel, 21, fast semisors undate)	(TremBLrel. 22, Last	ln.	Name=B1065G12.14;	Oryza sativa (japonica cultivar-group).	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;	Ehrhartoideae, Oryzeae, Oryza.	NCBI_TaxID=39947;	N MORN STATES	PubMed=12447438; DOI=10.1038/nature01184;	Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katavose Y.		Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,	Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,	Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,	Ikeno M., Iton S., Iton T., Iton Y., Iton Y., Iwabuchi A., Kamiya K., Karagawa W Matarizi C Wibuta & Waburahi W Wall T	Machita K., Machara T., Mizuno H. Mizubayashi T., Mukai V.	Nagasaki H., Nakashima M., Nakama Y., Nakamira M.	Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K, Shibata M.,	Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,	Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,	Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,	Yano M., Jiang J., Gojobori T.; "The genome semience and etwictive of vice observed 1".	Native 4.00.312_316 (2003)	EMBL: AP003791: BAB90532.1: -		SEQUENCE 72 AA; 7677 MW; 6A9368D674BE00A3 CRC64;	Query Match 100.0%; Score 29; DB 2; Length 72; Best Local Similarity 100.0%; Pred. No. 18;	ative 0;
RESULT QBRZ81	A D	55	Ę.	DE	2 8	SO	ပ္ပင္ပ	ဗ	ပ္ပ	ŏ	R P	2	æ	ð	æ	ð	& 2	¥ 8	5 2	æ	RA	æ	& :	\$;	8 E	Į.	E	DR	S	Que	Mat

1 TYAMH 5 ||||| 25 TYAMH 29 පු පු

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HU3H HUMAN

ID HV3H HUMAN STANDARD; PRT; 122 AA. AC P01769.

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE 1g heavy chain V-III region GA.

158 AA; 17289 MW; CIBIFB23AA6E930B CRC64;

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Nature 417:459-463(2002).
EMBL, AE011840, AAM36912.1; -.
IRROPAL12; KRNA synt I.
PROSITE; PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
                                                  Complete proteome. SEQUENCE 158 AA;
                                                                                      Query Match
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                                                                                                                                                                                                                KADA_PYRHO
                                                                                                   Best Loc
Matches
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Q9HZZ6
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KX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/4174599;

KA SILVA A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R., Quaggio R.B., Monteiro-Vitorello C.B., Van Sluya M.A., Almeida N.F., A Alves L.M.C., do Amaral A.M., Berrolini M.C., Camargo L.B.A., A Alves L.M.C., do Amaral A.M., Cardozo J., Chambergo F., Ciapina L.P., Caracolli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., A Caracolli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., Ratia V.B., Franco M.C., Greggio C.C., Gruber A., Rotauvama A.M., Kaih L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Ancorali B.C., Machado M.A., Madelra A.M., Martinez-Rosai N.M., Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H., Moreira L.M., Novo M.T.M., Okura V.K., Olivaira W.C., Olivaira V.R., Spinola L.A.P., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., Spinola L.A.P., Takita M.A., Truffi D., Tsai S.M., White F.F., Tezza R.I.D., Setubal J.C., Kitajima J.P.;

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Fromparison of the genomes of two Xanthomonas pathogens with differing thost specificities.",
                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                         Gарв
               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xanthomonas axonopodis [pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 29; DB 1; Length 122; 100.0%; Pred. No. 32; ative 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                  Ig-like.
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                        122 AA; 13166 MW; 74E5B6959E84100A CRC64;
                                                                                                              macroglobulin.
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02052; M3HUGA.
                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. SMART; SM00406; IGv; 1. Direct Protein sequencing; Immunoglobulin V region; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein XAC2050.
OrderedLocusNames=XAC2050,
                                                                                                                                                                            HSSP, P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003825; F:antigen binding; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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   sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
ses 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                              31 TYAMH 35
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                                         VCBI_TaxID=9606;
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                  SEQUENCE
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mase by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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                                        Gaps
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    2; Length 158;
                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 48, Last annotation update)
Adenylate kinaee (EC 2.7 4.3) (ATP-AMP transphosphorylase)
Name=adkA, OrderedLocusNames=PH1753;
Pyrococcus horikoshii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 17 ATP (Potential).
196 AA; 22413 MW; 26C834A1BE944D5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding; Complete proteome; Kinase; Transferase.
                                          ö
100.0%; Score 29; DB
100.0%; Pred. No. 42;
tive 0; Mismatches
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Matches 5; Conservative
                      Local Similarity 100.
                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF 00234; -; 1.
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                                                                                                                      132 TYAMH 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=53953;
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                                                                                1 TYAMH 5
                                                                                                                                                                                                                 KADA PYRHO
O59443;
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2007 ST: 85: 97 C
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SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed=10984043; DOI=10.1038/35023079;
MEDLINE-20437337; PubMed=10984043; DOI=10.1038/35023079;
MICKEY M.J. Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Fardy L.L., Coulter S.N., Folger K.R., Wa Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
Roizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
Complete genome sequence of Pseudomonas aeruginosa PAO1, an Nutre 406:599-964(2000). Pseudomonas aeruginoss. Bacteria, Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaces; Pseudomonas. NCBI_TaxID=287; EMBL; AR004711; AAGG6235.1; -.
PIR; B83290; B83290.
InterPro; IPR002781; DUP81.
Pfam; PP01925; DUF81.1 ..
Complete proteome; Hypothetical protein.
SEQUENCE 249 AA; 25989 MW; BB24827650F64D6A CRC64; 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
OrderedLocusNames=PA2847; 249 AA. Created) PRT; 01-MAR-2001 (TrEMBLrel. 16, PRELIMINARY; 01-MAR-2001 01-JUN-2003

ö 100.0%; Score 29; DB 2; Length 249; 100.0%; Pred. No. 67; 0; Indel8 Local Similarity 100. Query Match Best Loc Matches

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Q962C9 Q962C9;

Podocoryne carnea.
Bukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Anthomedugae,
Hydractiniidae, Podocoryne. 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Transcription factor Cnox4-Pc. 356 AA PRELIMINARY;

SEQUENCE FROM N.A.
MEDLINE=21349874; PubMed=11456446; DOI=10.1006/dbio.2001.0299;
Yanze N., Spring J., Schmidli C., Schmid V.;
"Conservation of Hox/ParaHox-related genes in the early development
a cnidarian.";

Dev. Biol. 236:89-98 (2001).

-1- SUBCELLULAR LOCATION: Nuclear (By similarity).

EMBL; AY036893, AAK63185.1; -.

HSSP; P090899; IKZ2.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005534; C:nucleus; IEA.

GO; GO:0005535; Homeodomain like.

InterPro; IPR001356; Homeodomain like.

InterPro; IPR00147; HTH lambrepressr.

Ffam; PP00046; Homeobox;

Pfam; PP00046; Homeobox;

InterPro; IPR00067; HTH lambrepressr.

PRINTS; PRO0024; HOMEOBOX.
PRINTS; PRO0031; HTHREPRESSR.
SMART; SMO0389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.

PROSITE; PS50071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 356 AA; 41170 MW; EAF5E2308D76C6BB CRC64; SKW

; 0 Query Match
100.0%; Score 29; DB 2; Length 356;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 5; Conservative 0; Mismatches 0; Indels

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Gaps

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481 AA. PRELIMINARY; Q6N097

G6N097;
05-JUL-2004 (TrEWBLrel. 27, Created)
05-JUL-2004 (TrEWBLrel. 27, Last sequence update)
05-JUL-2004 (TrEWBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686H20196.
Name-DKFZp686H20196;
Homo sapiens (Human).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606;

SEQUENCE FROM N.A.

TISSUE=Human esoplagus tumor;
TISSUE=Human esoplagus tumor;
TISSUE=Human cDNA Consortium;
Wamburt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
A Pobo G., Han M., Wiemann S.,
E Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
E Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
E SUBMITTE R640519; CAR45773.1; -.
RSSP; P01861; 1ADO.
RIGEPPO; IPR003106; Ig.
RIGEPPO; IRGO, IG.
RIGEPPO; IG.
RIGEPPO; IG.
ROMART; SM00406; IG.
ROMART; SM00406; IG.
ROMART; SM00406; IG.
ROMART; ROMO406; IG.
ROMART; ROMART; ROMO406; IG.
ROMART; ROMART; ROMA IG.

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RESULT 7

OGN097

OGN097

DT 05-JU

Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels Ampochetical protein. REOUENCE 481 AA; 52759 MW; 47220D9E64BDF9BB CRC64;

1 TYAMH 5 g ઠ

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Gaps

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50 TYAMH 54

QG8CN4 PRELIMINARY; PRT; 493 AA.
G6ECN4;
C5ECCT-2004 (TEMBLrel. 28, Created)
25-OCT-2004 (TEMBLrel. 28, Last sequence update)
25-OCT-2004 (TEMBLrel. 28, Last sequence update)
25-OCT-2004 (TEMBLrel. 28, Last annotation update)
Name=DKRZp68623209;
Name=DKRZp68623209;
Homo sapiens (Human).
Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; RESULT 8
968CN4
1D 068CC
AC 068CC
DT 25-00
DT 25

NCBI_TaxID=9606;

SEQUENCE FROM N.A

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25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Probable acetyl-coenzyme A synthetase.
Name=acs; OrderedLocusNames=DP0825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00154; AMPBINDING.
PROSITE; PS00455; AMP_BINDING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 TYAMH 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TYAMH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9V6J4
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                                       A Bloccker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C., Bloccker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C., A Bloccker H., Boecher M., Wiemann S.;

Submitted (Aug-2004) to the EMBL/GenBank/DDBJ databases.

In Submitted (Aug-2004) to the EMBL/GenBank/DDBJ databases.

R EMBL; CR79861; CR418705.1; -.

R InterPro; IPR00359; Ig.

InterPro; IPR00359; Ig.

InterPro; IPR003596; Ig.

R InterPro; IPR003596; Ig.

R InterPro; IPR003596; Ig.

R Ffam; PF00647; Ig. 4.

R SWART; SW00409; IG. 2.

R SWART; SW00406; IG. 1.

R ROSITE; PS50835; IG LIKE; 4.

R PROSITE; PS50835; IG LIKE; 4.
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Enterobacteriaceae, Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Score 29; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simoes R.C., Delicato B.R., Gaziri L.C.J., Vidotto M.C., Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases. BenBL; AS20856; ABA37381.1 ...
GOG, GO:0004252; F:serine-type endopeptidase activity; IEA. GO; GO:0006508; P:proteolysis and peptidolysis; IEA. InterPro; IPR009010; Peptidase S6. InterPro; IPR009003; Pept_Ser_Gys. Feam; PF02395; IGA1; 1.
PEAM: PF02395; IGA1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 493 AA; 54117 MW; A1E4F5ED3FA8AB40 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Tsh profesh (Fragment).
Escherichia coli.
                                The German cDNA Consortium;
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Matches 5; Conservative
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ID 06AQ19
AC 06AQ19;
DT 25-OCT-2004 (
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SEQUENCE
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(TrEMBLrel. 28, Created) (TrEMBLrel. 28, Last sequence update)

RESULT 10

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Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams H.D., Scherer S.E., Li P.W., Hookins R.A., Galle R.F.,
A manatides P.G., Scherer S.E., Li P.W., Hookins R.A., Hoderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Asbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B. B.C., Dunn P.,
A Fooler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
A Durkhin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleisehmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                              [1]
SEQUENCE FROM N.A.
STAIN=LEA'S 4 / DSM 12343;
PubMeda15305914;
PubMeda15305914;
Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
Rabus R., Lombardot T., Becker I., Amann J., Gellner K.,
Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
Klenk H.-P.;
Klenk H.-P.;
"The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
from permanently cold Arctic sediments.";
Environ. Macrobiol. 6:887-902(2004).
-1- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Desulfotalea psychrophila.
Bacteria, Proteobacteria, Deltaproteobacteria, Desulfobacterales,
Desulfobulbaceae, Desulfotalea.
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01-007-2002 (TrEMBLrel. 13, Created)
01-007-2002 (TrEMBLrel. 22, Last sequence update)
25-007-2004 (TrEMBLrel. 28, Last annotation update)
03915-PB (d127039p).
Name-brl-2; ORPNames-CG3915;
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Bukaryota, Metazoa; Arthropoda; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 29; DB 2; Length 544; 100.0%; Pred. No. 1.5e+02; rive 0; Mismatches 0; Indels
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GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
Interpro; IPR00873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
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Harrie N.L., Marvey D., Heimen T.J., Hernandez J.R., Houck J.,

A. Harrie N.L., Marvey D., Heimen T.J., Hernandez J.R., Houck J.,

B. Marrie D., Bousenow R.A., Howland T.J., Will Mr.H. Ingewom C.,

B. Marrie D., Housenow R.A., Howland T.J., Will Mr.H. Ingewom C.,

Liux N., Martel B., McTincoh T.C., McLed M.P., Marsen D.,

B. Marrie C., Milaihim N.W., Mobbar C., McDanie J.M., Malson D.L.,

B. Marsen S.M., My N., Murphy B., Murphy L., Murph D.M., Malson D.L.,

Palace C., Milaihim N.W., Mobbar C., Molded M.P., Schooler P., Shone B. M.

Reinert K., Martel D., Standers B., McTincoh T.C., McDanie D. M., Palace D.L.,

Palace E., Spaningen M., Stephenon M., Standers B., Shon He M.C.,

Shun B.C., Sider-Klame I. Simpon M., Standers B., Man He M.,

Shun B.C., Sider-Klame I. Simpon M., Standers B., Man He M.,

Shun B.C., Sider-Klame I. Simpon M., Standers B., Man He M.,

Shun B.C., Sider-Klame I. Simpon M., Standers B., Man He M.,

Shun B.C., Sider-Klame I. Simpon M., Standers B., Man He M.,

Shun B.C., Sider-Klame I. Simpon M., Standers B., Man He M.,

Shun B.C., Sider-Klame I. Simpon M., Standers B., Man He M.,

Shun B.C., Sider-Klame I. Simpon M., Standers B., Man He M.,

Shun B.C., Sider-Klame I. Simpon M., Standers B., Man He M.,

Shun B.C., Sider-Klame I. Simpon M., Standers B., Man H., Wang X.,

Milliams S.M., Macking M., Zhong W., Zhou W., Zhu S., Zhu X., Smith M.O.,

And Marking S.M., Macking M., Shun M., Wenter I.,

Man M., Man M., Shun M., Shun M., Man M., Man M.,

Man M., Man M., Man M., Man M., Man M., Man M., Man M.,

Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M.,

Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M.,

Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Man M., Ma
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Gaps
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O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 16, Last sequence update)
G1-UUN-2003 (TrEMBLrel. 24, Last annotation update)
G1-TUN-2003 (TrEMBLrel. 24, Last annotation update)
Aspergillus oryzae.
Bukarycta; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TAXID=5062;
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R EMBL; AE003820; AAF58429.3; -.
R HSSP; PO8581; 1RIW.
R HSSP; PO8581; 1RIW.
R PYBase; FEGN003791; Dr1-2.
R GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004713; F:Drotedn-tyrosine kinase activity; IEA.
GO; GO:0004713; F:Drotedn amino acid phosphorylation; IEA.
R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase.
R InterPro; IPR001245; Tyr_Dkinase.
R InterPro; IPR00245; Tyr_Dkinase.
R InterPro; IPR00366; MIF.
R PENDINS; RR00109; WIF; 1.
R PROSTIE; PS00109; PROTEIN KINASE DOM; 1.
R PROSTIE; PS00109; PROTEIN KINASE DOM; 1.
R PROSTIE; PS01019; MIF; 1.
R PROSTIE; PS05011; PROTEIN KINASE TYR; UNKNOWN_1.
R PROSTIE; PS05011; MIF; 1.
R KINASE TYR; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 29; DB 2; Length 6;
100.0%; Pred. No. 1.8e+02;
.ive 0; Mismatches 0; Indels
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ database EMBL, AX005477; AAG02575. 1. -
GO; GO:0004359; F:glutaminase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    690 AA; 76226 MW; 6546BE2499D8D43C CRC64;
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Last sequence update)
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Q9UVX9,
01-MAY-2000 (TEMBLrel. 13, L6
01-MAY-2000 (TEMBLrel. 13, L6
01-DEC-2001 (TEMBLrel. 19, L6
Glutaminase A.
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Best Local Similarity 100.
Matches 5; Conservative
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56 TYAMH 60
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423 TYAMH 427
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0946S1
1D 0946S
AC 0946S
AC 0946S
DT 01-MA
DT 0
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Matches
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Q9UVX9
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                                                                                        STRAIN-RIB40;
MEDLINE-20406523; PubMed=10952006;
MEDLINE-20406523; PubMed=10952006;
Kolbuchi K., Nagasaki H., Yuasa A., Kataoka J., Kitamoto K.;
Kolbuchi K., Nagasaki H., Yuasa A., Kataoka J., Kitamoto K.;
"Molecular cloning and characterization of a gene encoding glutaminase from Aspergillus oryzae.";
Appl. Microbiol. Biotechnol. 54:59-68(2000).
EMBL; AB029552; BAA86934.1; -.
SEQUENCE 690 AA; 76164 MW; E3D0B17841EEA00D CRC64;
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fowlpox virus (FPV).
Viruses; deDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Avipoxvirus
NCBI_TaxID=10261;
           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomacese; mitosporic Trichocomacese; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

BEDLINE-20193820, PubMed=10729156;

DOI=10.1128/JV1.74.8 .3815-3831.2000;

Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;

"The genome of fowlpox virus.";

J. WILCI. 74:3815-3831(2000).

-I. SIMILARITY: Contains 14 ANK repeats.
                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                  100.0%; Score 29; DB 2; Length 690; 100.0%; Pred. No. 1.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    V222_FOWPV STANDARD; PRT; 747 AA. 09J513]
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Putative ankyrin-repeat protein FPV222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00248; ANK; 15.
PROSITE; PS50297; ANK REP REGION; 1.
PROSITE; PS50089; ANK_REPEAT; 7.
ANK repeat; Hypothetical protein; Repeat.
REPEAT
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InterPro; IPR002110; ANK.
InterPro; IPR01810; F-box.
Pfam; PF00023; Ank; 13.
Pfam; PF00646; F-box; 1.
PRINTS; PR01415; ANKYRIN.
                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 5; Conservative
Aspergillus oryzae.
                                                                              SEQUENCE FROM N.A.
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                                           NCBI_TaxID=5062;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch):
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Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels (
                                                                                                                    Score 29; DB 1; Length 747;
Pred. No. 2.1e+02;
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Local Similarity 100.0%; Score 29; DB
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les 5; Conservative 0; Mismatches
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Title: Perfect score:

US-10-614-959-11 88 1 IISYDGSKKYYADSVKG 17 Sequence:

2105692 segs, 386760381 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

2105692 Total number of hits satisfying chosen parameters;

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp200s:*
4: geneseqp200s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
7: geneseqp2003ss:*
7: geneseqp2003bs:*
8: geneseqp2004ss:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aav79069 Anti-fact				Human	Single	Single	Adq96139 Single ch	Human E	Single	Add28319 Human her			6	6		-		3 Human	3 Human	1 Human	Human	6 Single	> 16::: >
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ALIGNMENTS

Ź AAY79069 standard; peptide; 17

12-JUN-2000 (first entry)

Anti-factor IX/IXa antibody H chain V domain CDR2 amino acid sequence

Complementarity determining region 2; CDR2; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome, AROS; arterial fibrillation; disseminated intravascular coagulopathy; DIC.

Homo sapiens.

WO200012562-A1.

39-MAR-2000

99WO-US019453. 26-AUG-1999;

98US-0098233P. 99US-0122767P. 28-AUG-1998; 03-MAR-1999;

(GETH) GENENTECH INC.

Kirchhofer D; Judice JK, Навв РЕ, Devaux B, Eaton DL, Adams CW, Suggett S;

4PI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

Claim 2; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 2 (CDR2) of the heavy chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXA/IXa a vitamin K dependent plasma serine procease that participates in the blood coaplation pathways. The Gla domain of factor IXa and its zymogen factor. IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

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Novel human antibody which binds human interleukin (IL)-4 receptor and is capable of inhibiting IL-4 induced biological activity, functions as IL-4 antagonist and is useful for treating septic arthritis, scleroderma.
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the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary angioplasty (PTCA), stroke, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular cosgulopathy (DIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; antibody; interleukin; IL-4; antagoniat; receptor; IL-4 receptor;
antiarthritic; dermatological; antiulcer; antinflammatory; cytostatic;
antistckling; immunosuppressive; tuberculostatic; ophthalmological;
antianemic; antithyroid.
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                                                                                                                                                                                                                    Length 17;
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; Pred. No. 3.2e-07;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                             ABB07230 standard; protein; 118 AA
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19-SEP-2000; 2000US-0065393.
15-EEB-2001; 2001US-00786934.
01-MAY-2001; 2001US-00847816.
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Best Local Similarity Loc.
Local 17; Conservative
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N-PSDB; ABA94330.
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ABB07230
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inhibiting an IL-4-induced biological activity. (I) is also useful for inhibiting both IL-4-induced biological activity in vivo in a human, and for treating septic arthritis in a human afflicted with septic arthritis. (I) is also used for treating conditions such as septic/reactive arthritis, dermathis herpetiformis, conditions such as septic/reactive arthritis, dermathis herpetiformis, curicaria (sepecially chronic idiopathic uriticaria), ulcers, gastric inflammation, mucosal inflammation, ulcerative colitis, Crohn's disease, inflammation, bwell disease, other disorders of the digestive system in which IL-4 plays a role (e.g. IL-4-induced inflammation of part of the gastrointestinal tract), conditions in which IL-4-induced barrier of disruption plays a role (e.g. conditions characterized by decreased epithelial barrier function in the lung or gastrointestinal tract), scleroderma, hypertrophic scarring, whipple's disease, benign prostate chyperplasia, IL-4-induced pulmonary conditions, allergic reactions to hyperplasia, IL-4-induced pulmonary conditions, allergic reactions to scleroderma, hypertrophic scarring, whipple's disease, benign prostate strauss syndrome, disease, sickle cell disease, benign prostate cucoimmune lymphoproliferative syndrome, autoimmune haemolytic anemia, strauss syndrome, drave's disease, pre-eclampsia, Sjogran's syndrome, caucoimmune lymphoproliferative syndrome, autoimmune blistering companies also find use as adjuvante to allergy immunocherapy and as canagonists also find use as adjuvante to allergy immunocherapy and as canagonists also find be beneficial in treating or preventing the disease.

THI response would be beneficial in treating or preventing the disease.

THI response would be beneficial in treating or preventing the disease.
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Pred. No. 4.1e-06;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6-2 heavy chain variable region
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2000US-0240816P.
2001US-0276248P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 118 AA;
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16-MAR-2001; 2
21-MAR-2001; 2
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Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell to proliferation and differentiation. The antibodies of the invention have proliferation, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be associated with aberrant expression of BLyS. They may also be and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumacoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and continued in the method of the invention

Sequence 248 AA;

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Gaps
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   98.9%; Score 87; DB 5; Length 248; 94.1%; Pred. No. 9.3e-06; arive 1; Mismatches 0; Indels
Query Match
Best Local Similarity 94.1
Matches 16; Conservative
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1 IISYDGSKKYYADSVKG 17

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ABP44905 standard; protein; 248

19-AUG-2002 (first entry) ABP44905;

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Human BLyS binding scFv SEQ ID 916.

BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulat; immunomodulatory; antirheumatic; antiAlDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

Homo sapiens

WO200202641-A1.

10-JAN-2002

16-JUN-2000; 2000US-0212210P. 17-OCT-2000; 2000US-0240B16P. 16-MAR-2001; 2001US-027624BP. 21-MAR-2001; 2001US-027379P. 25-MAY-2001; 2001US-0293499P.

(HUMA-) HUMAN GENOME SCI INC. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

ä Hilbert Vaughan T, Choi GH, Ruben SM,

WPI; 2002-114799/15

15-JUN-2001; 2001WO-US019110.

Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders. Claim 1; Page 1495-1496; 3148pp; English.

Сарв ö 98.9%; Score 87; DB 5; Length 248; 94.1%; Pred. No. 9.3e-06; ive 1; Mismatches 0; Indels 16; Conservative Best Local Similarity Query Match Matches

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17 1 IISYDGSKKYYADSVKG

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ABP44903 standard; protein; 248 AA.

(first entry) 19-AUG-2002

fuman BLyS binding scFv SEQ ID 914.

BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tummour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive, immunostimulator; immunosuppressive, immunostimulator; immunosimulator; antitheumatic; antiAlDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

10-JAN-2002.

Choi GH, Vaughan T, Hilbert D; Barash SC, Ruben SM,

WPI; 2002-114799/15

This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell to tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antithemmatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be associated with aberrant sypression of BLyS. They may also be and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune (AlDS). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of

Sequence 248 AA;

RESULT 5 ABP44903

Homo sapiens

VO200202641-A1.

15-JUN-2001; 2001WO-US019110.

16-JUN-2000, 2000US-0212210P. 17-CCT-2000, 2000US-0240B16P. 16-MAR-2001, 2001US-0276248P. 21-MAR-2001, 2001US-0293499P.

(HUMA-) HUMAN GENOME SCI INC. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant albys expression and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP41920-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
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Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                              Claim 1; Page 1492-1493; 3148pp; English.
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19-DEC-2001; 2001US-0340817P.
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                               the invention
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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 13q34 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFv8) derived, preferably, from the variable composition to factor of early propertied. The variable composition of either human, murine, rat or monkey BLyS. The fragment thereof, of either human, murine, rat or monkey BLyS. The composition, disquests and prognosis of diseases related to the eaberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders concluding myserbhaia and rheumatoid archritis, infectious diseases such as ALDS and proliferative disorders including leukaemia, carcinoma and concluding such as and multiple sclerosis, inflammatory actions and contintial and proliferative disorders including leukaemia, carcinoma and contintial and proliferative disorders including leukaemia, carcinoma and contintial and proliferative disorders including leukaemia, carcinoma and contintial and such as anticheumatic, antiallergic and cytostatic. This contypeptide sequence is a single chain antibody that binds BLyS of the invention. NOTE: The sequence data for this patent did not form part of directely from WIPO at ftp.wipo.int/published pot_sequences.
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19-DEC-2001; 2001US-0340817P.
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Matches 16; Conservative
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Example 1; SEQ ID NO 916; 394pp; English

Sequence 248 AA;

Gaps ó 98.9%; Score 87; DB 7; Length 248; 94.1%; Pred. No. 9.3e-06; Live 1; Mismatches 0; Indels 16; Conservative Sest Local Similarity Query Match Matches

99 1 IISYDGSKKYYADSVKG

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ADG96139 standard; protein; 248 AA.

11-MAR-2004 (first entry)

Single chain antibody that immunospecifically binds BLyS SeqID 1323.

antibody, B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; cardinoma; lymphoma; antitheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.

Unidentified

WO2003055979-A2.

10-JUL-2003

14-NOV-2002; 2002WO-US036496

16-NOV-2001; 2001US-0331469P.

(HUMA-) HUMAN GENOME SCI INC.

Choi GH, Vaughan TJ, Hilbert D; Ruben SM, Barash SC,

WPI; 2003-505530/47.

Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.

Example 1; SEQ ID NO 1323; 394pp; English.

This invention relates to novel antibodies that immunospecifically bind CC to B lymphocyte stimulator (BbyS). The BbyS gene has been mapped to chromosome 1344 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single companies (screws) derived, preferably, from the variable companies (screws) derived, preferably, from the variable companies (screws) derived, preferably, from the variable companies of either human, murine, rat or monky BbyS. The companies of either human, murine, rat or monky BbyS. The companies and prognosis of diseases related to the sact and the detection, diagnosis and prognosis of diseases related to the sact and the compositions are useful for identifying immune diseases including myasthenia gravis and multiple sclerosis, inflammatory composited and multiple sclerosis, inflammatory and proliferative diseorders including leukemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various continitiammatory, antiasthmatic, antiathritic, neuroprotective, continitialmanalismuscomy and such as single chain antibody that binds BbyS of the convertion. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format.

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Seguence 248 AA;

Gaps . 0 Query Match 98.9%; Score 87; DB 7; Length 248; Best Local Similarity 94.1%; Pred. No. 9.3e-06; Matches 16; Conservative 1; Mismatches 0; Indels

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1 IISYDGSKKYYADSVKG 17

ð 셤 RESULT 9 ABP45103

ABP45103 standard; protein; 251 AA.

(first entry) 19-AUG-2002

Human BLyS binding scFv SEQ ID 1114.

BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulatic; immunosuppressive; immunostimulatic; immunosuppressive; antithematic; antithematic; succine; cancer; immunostimulatic; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

Homo sapiens

WO200202641-A1.

10-JAN-2002.

15-JUN-2001; 2001WO-US019110.

16-JUN-2000; 2000US-0212210P. 17-OCT-2000; 2000US-0240B16P. 16-MAR-2001; 2001US-027624BP. 21-MAR-2001; 2001US-027379P. 25-MAY-2001; 2001US-0293499P.

(HUMA-) HUMAN GENOME SCI INC. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

ä Choi GH, Vaughan T, Barash SC, Ruben SM,

Antibodies against B Lymphocyte Stimulating polypeptides, useful for the

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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell collision and differentiation. The antibodies of the invention have proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, inheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (cvID) and acquired immunodeficiency syndrome (AIDS)). ABP47228 represent the antibodies and fragments of the antibodies described in the method of
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Pred. No. 9.4e-06;
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diagnosis and treatment of cancers and immune disorders.
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                                     Claim 1; Page 1731-1732; 3148pp; English.
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es 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 251 AA;
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Matches
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cc to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 19434 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvB) derived, preferably, from the variable chary CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The creament invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As uch, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders as ALDS and proliferative disorders including leakeamia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various crivities such as antirheumatic, antiallergic and cytostatic. This antinflammatory, antiallergic and cytostatic. This antinflammatory as a single chain antibody that binds BLyS of the invention. NoTE: The sequence data for this patent did not form part of disorder antiple of properties the printed specification, but was obtained multiple and cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor;
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29-APR-2002; 2002US-0376408P.
27-SEP-2002; 2002US-0414053P.
25-NOV-2002; 2002US-0428807P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 251 AA;
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The present invention describes a human heterodimeric antibody (I) (fragment) having a binding affinity of at least 1x10-8 M to the protective antigen of Bacillus anthracis or a molecule involved in anthrax infection that blocks binding of the antigen or molecule to cell receptors, edema factor and lethal factor. (I) has virucide and antibacterial activities, and can be used in immunotherapy. The antibodies (I) are useful as anti-toxins or anti-infectives with respect to infective agents, such as anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The present sequence represents a human heterodimeric antibody heavy chain of the present invention. Claim 11; SEQ ID NO 97; 67pp; English.

Sequence 135 AA;

Query Match
97.7%; Score 86; DB 7; Length 135;
Best Local Similarity 94.1%; Pred. No. 6.8e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 1 IISYDGSKKYYADSVKG 17

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ABB07186 standard; protein; 119 AA. RESULT 12

(first entry) 13-MAR-2002 ABB07186;

sHigM22 heavy chain variable region clone B sequence.

Neuromodulatory; central nervous system; CNS; sHIGM22; LYM 22; AKJR4; ebvHigM MsI19D10; ebv HIgM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide; antiparkinsonian; neuroprotective; nootropic; vulnerary.

Ношо

40200185797-A1.

15-NOV-2001

30-MAY-2000; 2000WO-US014902.

10-MAY-2000; 2000US-00568351

Rodriguez M, Miller DJ, Pease

(MAYO-) MAYO FOUND MEDICAL EDUCATION RES.

WPI; 2002-066596/09. N-PSDB; ABA94243.

Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious encephalomyelitis.

Claim 23; Fig 17; 219pp; English.

The invention provides a neuromodulatory agent (1) capable of promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system (CNS). (I) is capable of inducing remyelination, promoting callular proliferation of glial calls, and promoting Ga2+ signaling with oligodendrocytes. An humanised antibody to (1) can be selected from antibody sHIGMS2 (LYM 22), ebvHigM MBI19D10, ebv HigM cB2bG8, AKGN4, CB21E12, CB2LE7 or MBI19ES. (I) is useful for stimulating remyelination of CNS axons, stimulating proliferation of glial cells in

CC CNS axons, or treating demyelinating disease of CNS in a mammal in need of such therapy. (I) is capable of binding to structures and cells within CC CNS. (I) is preferably useful for treating a demyelinating disease of CNS of a mouse infected with Strain DA of Theiler's murine encephalomyelitis of a mouse infected with Strain DA of Theiler's murine encephalomyelitis (TMEV) or for treating a human being having multiple sclerosis, or a post-or human or domestic animal with a viral demyelinating disease, or a post-or estimulating the proliferation of gilal cells from mixed cell culture. (I) is also useful for stimulating remyelination of CNS axons. The antibodies contains that causes demyelination or toher neurodegenerative condition in subject. Methods where (I) is administered to a patient are useful cor treating multiple aclerosis, Parkinson's disease, Alzheimer's disease, amyortophic lateral sclerosis (ALS), a viral demyelinating chisease, CNS diseases, and other conditions in the CNS where nerves are damaged as by trauma. The present sequence represents the sHigM22 heavy condition viraliable region clone B amino acid sequence

Sequence 119 AA;

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Gaps ; 0

0; Gapa 96.6%; Score 85; DB 5; Length 119; 94.1%; Pred. No. 8.6e-06; ive 1; Mismatches 0; Indels 16; Conservative Local Similarity Query Match Best Loc Matches

.. 0

RESULT 13 ABO33850

ABO33850 standard; peptide; 17 AA.

(first entry) 18-SEP-2003

Anti-GPI-antibody heavy chain complementarity determining region #10.

Human; anti-glucose-6-phosphate isomerase-antibody; immunopolypeptide; anti-GPI-antibody; GPI; glucose-6-phosphate isomerase; autoimmune disease; rheumatoid arthritis; heavy chain variable region; VH; complementarity determining region; CDR.

US2002146753-A1.

.0-OCT-2002.

06-APR-2001; 2001US-00828708.

06-APR-2001; 2001US-00828708. (BURT/) DITZEL H. (BURT/) BURTON D R. (SCHA/) SCHALLER M.

Schaller M; Burton DR, Ditzel H,

WPI; 2003-521517/49.

Immunopolypeptide for diagnosis and treatment of human autoimmune disease, e.g., human rheumatoid arthritis, comprises a polypeptide that binds to human glucose-6-phosphate isomerase.

Claim 3; Fig 4A; 47pp; English.

The invention describes an immunopolypeptide comprising a polypeptide that binds to human glucose-6-phosphate isomerase (GPI). The methods a compositions are used for disgnosis and treatment of human autoimmune disease, e.g., human rheumatoid arthritis. This is the amino acid sequence of human anti-GPI-antibody heavy chain variable region

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Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious encephalomyelitis.
                                                               Neuromodulatory; central nervous system; CNS; sHIGM22; LYM 22; AKJR4; ebvHigM MsI19D10; ebv HIGM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide; antiparkinsonian; neuroprotective; nootropic; vulnerary.
                                          sHigM22 heavy chain variable region clone A sequence
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                                                                                                                                                                                                                                                                                                                                                                                 Claim 23; Fig 17; 219pp; English
                                                                                                                                                                                      30-MAY-2000; 2000WO-US014902.
                                                                                                                                                                                                              10-MAY-2000; 2000US-00568351
                      (first entry)
                                                                                                                                                                                                                                                            Miller DJ,
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                                                                                                                    Homo sapiens
                      13-MAR-2002
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 ABB07169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes an immunopolypeptide comprising a polypeptide that binds to human glucose-6-phosphate isomerase (GPI). The methods and compositions are used for diagnosis and treatment of human autoimmune disease, e.g., human rheumatoid arthritis. This is the amino acid sequence of human anti-GPI-antibody heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunopolypeptide for diagnosis and treatment of human autoimmune disease, e.g., human rheumatoid arthritis, comprises a polypeptide that binds to human glucose-6-phosphate isomerase.
                                                                                                                                                                                                                                                                           anti-glucose-6-phosphate isomerase-antibody; immunopolypeptide;
                                                                                                                                                                                                                                                                                        anti-GPI-antibody, GPI; glucose-6-phosphate isomerase;
autoimmune disease; rheumatoid arthritis; heavy chain variable region;
                                                                       Gaps
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                                                Score 84; DB 7; Length 17;
Pred. No. 1.4e-06;
2; Mismatches 0; Indels
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    complementarity determining region
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                                                 Query Match
Best Local Similarity 88.2%;
Matches 15; Conservative
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(SCHA/) SCHALLER M.
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les 15; Conser
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Pease LR;

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The invention provides a neuromodulatory agent (I) capable of promoting central nervous system (CNS). (I) is capable of inducing remyelination, central nervous system (CNS). (I) is capable of inducing remyelination, central nervous system (CNS). (I) is capable of inducing remyelination, compared antibody to (I) can be signaling with oligodendrocytes. An humanised antibody to (I) can be selected from antibody shights? (LMM 22). ebviligh MeIDBIO, ebv High CS achected from antibody shights? (LMM 22). ebviligh MeIDBIO, ebv High CS axons, or treating demyelinating proliferation of glial cells in cremyelination of CNS axons, stimulating proliferation of glial cells in constant therapy. (I) is capable of binding to structures and cells within constitution of constant and the strain BA of Theiler's murine encephalomyelitis (TMEV) or for treating a human being having multiple sclerosis, or a constant disease of CNS. (I) is also useful for an in vitro method of stimulating the proliferation of glial cells from mixed cell culture. (I) can useful for stimulating remyelination of CNS axons. The antibodies are useful for preventing infection by a bacterium, virus or like conting in the cause demyelinating remyelination of CNS axons. The antibodies conting the selecosis, Parkinson's disease, Alzheimer's condition of disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating demyelinating changes are disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating demyelinating energed and energed as by trauma. The present sequence represents the shighZ2 heavy
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88.2%; Pred. No. 1.3e-05;
iive 2; Mismatches 0;
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ABB07169 standard, protein, 119 AA,

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5.1.6 Compugen Ltd.		; Search time 33.4688 Seconds (without alignments) 37.917 Million cell updates/sec				51354			<pre>l8sued Patents AA:* /cgn2_6/ptodata/1/iaa/5A_COMB.pep:* /cgn2_6/ptodata/1/iaa/5B_COMB.pep:* /cgn2_6/ptodata/1/iaa/6A_COMB.pep:* /cgn2_6/ptodata/1/iaa/6B_COMB.pep:* /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*</pre>	No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.		De					•							, www.	วั
5.1.6 Compue		Searchithout			œ	ters:			COMB.p COMB.p COMB.p COMB.p COMB.p	icted e of t score			7-11	7-16 7-20)B-36	B-108	A-167	US-08-211-202-141 US-08-545-809A-115 US-08-331-398A-46	B-46 A-46	-46	1.38	9-e	A-96 A-80 B-77	B-111 B-16	7
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Sequence 102, App Sequence 108, App Sequence 110, App Sequence 102, App Sequence 108, App Sequence 110, App Sequence 11, Appl Sequence 12, Appl Sequence 13, Appl Sequence 2, Appl Sequence 10, Appl Sequence 21, Appl Sequence 11, Appl Sequence 81, Appl	dies	Length 17; Indels 0; Gaps 0; odies
US-09-456-090A-102 US-09-456-090A-110 US-09-451-234-102 US-09-453-234-102 US-09-453-234-110 US-09-453-234-110 US-08-862-124-17 US-08-862-124-17 US-09-560-198A-12 US-09-560-198A-12 US-09-464-840B-113 US-09-461-198A-1 US-09-560-198A-1 US-09-560-198A-1 US-09-560-198A-1 US-09-560-198A-1 US-09-560-198A-1 US-09-560-198A-1 US-08-560-198A-1 US-08-560-198A-1 US-08-560-198A-1 US-08-560-198A-1 US-08-560-198A-1 US-08-560-198A-1 US-08-560-198A-1 US-08-60-108A-1	ALIGNMENTS SSULT 1 5-09-383-667-11 Sequence 11, Application US/09383667 Patent No. 6664295 GENERAL INFORMATION: APPLICANT: Adams, Camelia W. APPLICANT: Adams, Camelia W. APPLICANT: Adams, Camelia W. APPLICANT: Baron, Dan L. APPLICANT: Hass, Philip E. APPLICANT: Hass, Philip E. APPLICANT: Sugget, Daniel APPLICANT: Sugget, Shelley TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies FILE REFERENCE: Pic61R2 CURRENT APPLICATION NUMBER: US 60/098,233 EARLIER PLING DATE: 1999-03-03 EARLIER PLING DATE: 1999-03-03 NUMBER OF SEQ ID NOS: 32 SEQ ID NO 11 TYPE: PRT ORGANISM: Home sapiens -09-383-667-11	re 88; DB 4; d. No. 1.3e-07; ismatches 0;
2225 2225 2225 2225 2225 2225 2225 222	ESULT 1 S-09-383-667-11 Squence 11. Application US/09383667 Patent NO. 6624295 GENERAL INFORMATION: APPLICANT: Adams, Camelia W. APPLICANT: Beton, Dan L. APPLICANT: Baton, Dan L. APPLICANT: Taton, Dan L. APPLICANT: Widle, J. Kevin APPLICANT: WIDLE, J. Shelley TITLE OF INVENTION: Human Anti-Fact CURRENT FILING DATE: 1999-08-26 EARLIER APPLICATION NUMBER: US 60/0 EARLIER FILING DATE: 1999-08-26 EARLIER FILING DATE: 1999-03-03 SEQ ID NO 11 LENGTH: 17 TYPE: PRT ORGANISM: Homo sapiens	100 vativ. YYADS' YYADS' YYADS' TILL YYADS' TILL TILL TILL E. TREVIT TO DE STANDEN
9 9 2 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1.11 (, Application (6.24295) CORMATION: Adams, Camel Davaux, Brig Davaux, Brig Davaux, Brig Davaux, Dan II Hass, Philip Judice, J. Kirchhofer, Shenner Perication Num Perication Num Perication Num Perication Num Ling Dare: 19 Perication Num Ling Da	Similarity 7; Conser 11SYDGSKK 1 11SYDGSKK 1 11SYDGSKK 624295 6624295 6624100; Applicat 6624295 Faton, Dai Hass, Phi Hass, Phi Hass, Phi Kirchhofe, J Kirchhofe, Suggett, E NVENTION:
88 B B B B B B B B B B B B B B B B B B	SULT 1 5-09-383-667-11 Sequence 11, Application Patent No. 6624295 GENERAL INFORMATION: APPLICANT: Adams, Camel APPLICANT: Baton, Dan LAPPLICANT: Baton, Dan LAPPLICANT: Baton, Dan LAPPLICANT: Suggett, She TITLE REFERENCE: P1661R2 CURRENT APPLICATION NUM FILE REFERENCE: 19661R2 CURRENT APPLICATION NUM EARLIER PILING DATE: 1968R2 CURRENT APPLICATION NUM EARLIER PILING DATE: 1968R2 CURRENT RILING DATE: 1968R2 CURRENT RILING DATE: 1968R2 CURRENT RILING DATE: 197 EARLIER PILING DATE: 197 EARLIER PILING DATE: 197 TYPE: PRT CURRENT: 17	Query Match Best Local Similari Matches 17, Cons 1 IISYDGS, 1 IISYDGS,
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-09-383-6 ; Sequence ; Patent No ; GENERAL II APPLICAN ; APPLICAN	Query Match Best Local Sim Matches 17; Qy 1 II Db 1 II Db 1 II RESULT 2 US-09-383-667-18 Sequence 18, A PELICANT: Ad APPLICANT: Be APPLICANT: Be APPLICANT: Be APPLICANT: GA APPLICANT:

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GEOUGH OF A PAPLICATION US/09424840B

Sequence 95, Application US/09424840B

Sequence 95, Application US/09424840B

Sequence 95, Application US/09424840B

GENERAL INCOMMATION:
APPLICANT: Becher, Robert F. A.
APPLICANT: Becher, Robert F. A.
TILLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049

CURRENT APPLICATION NUMBER: US/09/424,840B

PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03

PRIOR FILING DATE: 1999-12-12

PRIOR FILING DATE: 1997-12-12

PRIOR FILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-44-840B-36

JG-09-44-840B-36

Sequence 36, Application US/09424840B

Patent No. 6790338

GENERAL INFORMATION:
APPLICANT: Berchtold, Peter
APPLICANT: Berchtold, Peter
PITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
CURRENT APPLICATION NUMBER: US/09/424,840B

CURRENT FILING DATE: 1999-12-03
PRIOR PAPLICATION NUMBER: DE 19820663.1
PRIOR PELICATION NUMBER: DE 1975227.7
PRIOR PLING DATE: 1997-12-12
PRIOR PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128

SOFTWARE: Patentin Version 3.1
SEQ ID NO 36

SEC IN NO 36
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                                                                                                                                                                                                                                                                                            Length 17;
                                                                                                                                                                                                                                                                                          ch 93.2%; Score 82; DB 4; Le
1 Similarity 100.0%; Pred. No. 1.2e-06;
16; Conservative 0; Mismatches 0;
CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 20
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IISYDGSKKYYADSVKG 17
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Best Local Similarity 88.2
Matches 15; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-424-840B-36
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; Sequence 16, Application US/09383667
; Patent No. 6624295
; GENERAL MO. 6624295
; GENERAL INFORMATION:
APPLICANT: Adams, Camelia W.
APPLICANT: Baton, Dan L.
APPLICANT: Hass, Philip E.
APPLICANT: Hass, Philip E.
APPLICANT: Sagett, Shelley
TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
FILE REFERENCE: P1661R2
CURRENT APPLICATION NUMBER: US/09/383,667
CURRENT APPLICATION NUMBER: US 60/098,233
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER APPLICATION NUMBER: US 60/122,767

EARLIER PILING DATE: 1999-03-03
; NUMBER OF SEO ID NOS: 32
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Patent No. 6624295

GENERAL INFORMATION:

APPLICANT: Dames, Camelia W.

APPLICANT: Baton, Dan L.

APPLICANT: Hase, Philip E.

APPLICANT: Judde, J. Kevin

APPLICANT: Sugget, Shelley

TILE OF INVENITON: Human Anti-Factor IX/IXa Antibodies

FILE REFERENCE: P1661R2

CURRENT APPLICATION NUMBER: US/09/383,667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.2%; Score 82; DB 4; Length 17; 88.2%; Pred. No. 1.2e-06;
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                                   CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 18
LENGTH: 17
            CURRENT APPLICATION NUMBER: US/09/383,667
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Matches 15; Conservative
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                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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US-09-383-667-20
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US-09-424-840B-108
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| Patent No. 6790938
| GENERAL INFORMATION:
| APPLICANT: Berchtold, Peter |
| CURRENT APPLICATION NUMBER: US/09/424,840B |
| CURRENT FILING DATE: 1999-12-03 |
| PRIOR PPLICATION NUMBER: DE 19755227.7 |
| PRIOR APPLICATION NUMBER: DE 19755227.7 |
| PRIOR PLING DATE: 1997-10-12 |
| PRIOR APPLICATION NUMBER: DE 19723904.8 |
| PRIOR PILING DATE: 1997-06-06 |
| SOFTWARE: PatentIn Version 3.1 |
| SEQ ID NO 97 |
| LENGTH: 17
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| Patent No. 6790938
| GENERAL INFORMATION:
| APPLICANT: BEACHLOID, Peter |
| APPLICANT: BECCHLOID, ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES |
| FILE REFERENCE: 100564-09049 |
| CURRENT APPLICATION NUMBER: US/09/424,840B |
| PRIOR PELING DATE: 1999-12-03 |
| PRIOR PELING DATE: 1998-05-08 |
| PRIOR PILING DATE: 1997-12-12 |
| PRIOR APPLICATION NUMBER: DE 1975227.7 |
| PRIOR PILING DATE: 1997-06-06 |
| NUMBER OF SEQ ID NOS: 128 |
| SEQ ID NO 108 |
| LENGTH: 17
                                                                                                                                                                  Ouery Match
93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels
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Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1
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SOFTWARE: Patentin version 3.1
SEQ ID NO 95
LENGTH: 17
                                                                                        ; ORGANISM: Homo sapiens
US-09-424-840B-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT; ORGANISM: Homo Bapiens
US-09-424-840B-97
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ORGANISM: Homo saptens
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US-09-424-840B-97
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Gарв
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APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
APPLICANT: BALER, Michael
APPLICANT: USSPERS, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: Borun
STREET: Galou Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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CUGNINIA: USA
CUGNINIA: USA
CUGNITER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IS PC COMPATIBLE
COMPUTER: PAGENINIA: DEC COMPATIBLE
COMPUTER: PAGENINIA: DEC COMPATIBLE
COMPUTER: PAGENINIA: DEC COMPATIBLE
SOFTWARE: PATENINIA DATA:
APPLICATION UNMBER: US/08/211,202
CLASSIFICATION: A35
FILING DATE: 23-SEP-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATE: APPLICATION NUMBER: GB 9206312.6
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 15-MAR-1992
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 34-MAR-1992
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 34-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: DATA W. CLOUGH
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 31,107
       Length 17;
                                                          1; Indels
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Pred. No. 7.3e-06;
  Score 82; DB 4; Pred. No. 1.2e-06; 1; Mismatches 1
                                                                                                                                                                                                                                                                        Sequence 118, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
                                                                                                  1 IISYDGSKKYYADSVKG 17
                                                                                                                                 1 VISYDGSNKYYADSVKG 17
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Query Match
Best Local Similarity 88.2%;
Matches 15; Conservative
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Best Local Similarity
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TOPOLOGY: linear MOLECULE TYPE: protein
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APPLICANT: Holliger, Kasper
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Boner, Timochy
TITLE OF INVENTION Methods for Producing Members of Specific Binding Pairs
FILE REPERENCE: 213839-00013
CURRENT APPLICANTON NUMBER: US/09/726,219A
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   Gaps
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93.2%; Score 82; DB 4; Length 115;
Best Local Similarity 88.2%; Pred. No. 8.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels
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Patent No. 5565312
GENERAL INFORMATION:
APPLICANT: HOGGENBOOM, Hendricus Renerus Jacobus Matteus
APPLICANT: BAIER, Michael
   Indels
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR PLILING DATE: 1990-0-10
PRIOR PLILING DATE: 1990-10-19
PRIOR PELING DATE: 1990-10-19
PRIOR PELING DATE: 1990-10-19
PRIOR PLILING DATE: 1990-10-19
PRIOR FILING DATE: 1990-10-19
PRIOR FILING DATE: 1990-10-19
PRIOR PLILING DATE: 1991-03-06
PRIOR PLILING DATE: 1991-03-06
PRIOR PLILING DATE: 1991-03-06
PRIOR PLILING DATE: 1991-03-06
PRIOR PLILING DATE: 1991-07-10
                                                                                                                                                                                                                                                                                            Sequence 167, Application US/09726219A
Patent No. 6806079
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Hoogenboom, Hendricus
Griffiths, Andrew
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                                                                                                                 SO VISYDGSNKYYADSVKG 66
                                                                        1 IISYDGSKKYYADSVKG 17
          15; Conservative
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ORGANISM: Homo sapiens
US-09-726-219A-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-211-202-141
             Matches
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APPLICANT: SEPERS. ADMINISTRY OF CHARGOTY PULL
TITLE OF INVENTION: CREDINGES: 144
COMMESSEE: David W. Clough, Marchall O'TOole Genetein Murray & ADDRESSEE: David W. Clough, Marchall O'TOole Genetein Murray & ADDRESSEE: David W. Clough, Marchall O'TOole Genetein Murray & ADDRESSEE: David W. Clough, Marchall O'TOole Genetein Murray & ADDRESSEE: David W. Clough, Marchall O'TOole Genetein Murray & ADDRESSEE: David W. Clough, Marchall O'TOole Genetein Murray & ADDRESSEE: David W. Clough, Marchall O'TOOL Genetein Murray & CONFINENT CALCAGO O'CONFINENT INSO O'CONFINENT O'CONFINE
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us-10-614-959-11.rai

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INCOME. Application US/08331398A

Fatence 46, Application US/08331398A

Fatence 10. 5608039

GENERAL INFORMATION:

APPLICANT: Pastan. Ira

APPLICANT: PitzGerald, David

APPLICANT: Brinkmann, Ulrich

APPLICANT: Single Chain B3 Antibody Fusion Proteins

ITILE OF INVENTION: and Their Uses (as amended)

NUMBER OF SEQUENCES:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Street Plaza

CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.2%; Score 82; DB 3; Length 117; 88.2%; Pred. No. 8.8e-06;
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COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAETALIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
                                                                                                                                                                                                              MEDION TIPE:
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: PastSEQ for Windows95
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
FRION APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING APPLICATION NUMBER: PCT/JP93/00603
ATTORNEY AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEX: 200154
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LEMOTH: 117 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IISYDGSKKYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 VISYDGSNKYYADSVKG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 93.2
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                           COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-115
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WESULT 14
US-08-311-397B-46

Sequence 46, Application US/08331397B

Patent No. 5981726

GENERAL INFORMATION:
FARENAL INFORMATION:
FARENAL INFORMATION:
FARENAL INFORMATION:
CHINERYLOW:
FITLE OF INVENTION:
FARENAL SAPERATION:
FARENAL SAPERATION DATE:
FILING DATE:
FARENAL SAPERATION DATE:
FARENAL SAPERA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:

NAME/KEY: Protein

LOCATION: 1..119

OTHER INFORMATION: /note= "Human fetal immunoglobulin

COTHER INFORMATION: 56Pl'CL Variable Heavy chain (V-H)"
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: HUNTER, TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPRAX: (415) 543-9600
TELEPRAX: (415) 543-9603
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
SEGUENCE CHARACTERISTICS:
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
STRANDENNES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REPERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IISYDGSKKYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
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Search completed: October 14, 2005, 16:22:00 Job time : 33.4688 secs
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Sequence 46, Application US/08759804A

Parent No. 590296

GENERAL INFORMATION: Ira
APPLICANT: Fastan, Ira
APPLICANT: FitzGerald, David J.
APPLICANT: FitzGerald, David J.
APPLICANT: Patinamn, Ulrich
APPLICANT: Promeed and Townsend and Uses Thereof
NUMBERSON EN ADDRESS:
ADDRESSER: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
CUNTRY: USA
ZITP: Q111:73334

CUNTRY: USA
ZITP: P411:7334

CONPUTER READABLE FORM:
MEDIUM TYPE: PC-DOS/MS-DOS
SOUTHARE: Patentin Release #1.0, Version #1.30
CUNTRENT APPLICATION NATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 30-SEP-1991
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
APPLICATION NUMBER: US 08/331,398
FILING DATE: 30-SEP-1991
APPLICATION NUMBER: US 08/759,804
FILING DATE: 30-SEP-1991
APPLICATION NUMBER: US 08/759,804
FILING DATE: 30-SEP-1991
APPLICATION NUMBER: US 08/759,804
ATTORNEY/AGENT INFORMATION:
NAME: Weber: Ellen L.
RESERRICE/DOCKET NUMBER: US 08/757,331
FILING DATE: 30-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Weber: Ellen L.
RESERRICE/DOCKET NUMBER: US 08/759,804
TELEPHONE: GHARATION INFORMATION:
NUMBER: Weber: APPLICATION NUMBER: US 08/759,804
TELEPHONE: GHARATION INFORMATION:
NUMBER: Weber: APPLICATION NUMBER: US 08/759,804
TELEPHONE: GHARATION INFORMATION:
NUMBER: US 05/750
ATTORNEY/AGENT NUMBER: US 08/750
ATTORNEY/AGENT NUMBER: US 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.2%; Score 82; DB 2; Length 119; 88.2%; Pred. No. 8.9e-06;
                                                                                                                                                                                                                                                                  ) NAME/KEX: Protein

; LOCATION: 1.119

; OTHER INFORMATION: /note= "Human fetal immunoglobulin

; OTHER INFORMATION: 56Pl'CL Variable Heavy chain (V-H)"

US-08-331-3978-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IISYDGSKKYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SO VISYDGSNKYYADSVKG 66
                                                                                           LENGTH: 119 amino acide
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 119 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 88.29
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-08-759-804A-46
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Gaps
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0
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                                                                                                           /note= "Human fetal immunoglobulin
56Pl'CL Variable Heavy chain (V-H)"
                                                                                                                                                                                                                                                                      1 IISYDGSKKYYADSVKG 17
                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                    MAMEKEY: Protein
COCATION: 1.119
OTHER INFORMATION: /
OTHER INFORMATION: 5
US-08-759-804A-46
STRANDEDNESS
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RESULT 1
US-10-989-462-300
                                                                                                                                                                         October 14, 2005, 16:20:10; Search time 120.859 Seconds (without alignments) 58.615 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
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22: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1859788 seqs, 416717961 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                         US-10-614-959-11
88
1 IISYDGSKKYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 300, App Sequence 262, App Sequence 914, App Sequence 916, App Sequence 1323, Ap Sequence 914, App Sequence 1114, Ap Sequence 1114, Ap Sequence 1114, Ap Description US-10-989-462-300 US-10-989-465-262 US-09-880-748-914 US-09-880-748-1323 US-10-293-418-914 US-10-293-418-1323 US-10-293-418-1323 US-10-293-418-1313 US-10-293-418-1114 US-10-293-418-1114 US-10-989-462-276 Query Match Length DB Score 87 87 87 87 87 87 87 87

Sequence 97, Appl	Sequence 97, Appl	Sequence 24, Appl	Sequence 24, Appl	Sequence 10, Appl	Sequence 10, Appl								Sequence 1690, Ap		Sequence 62, Appl	48	46	ý	2	39	51	81	36	95	97	70	23	Ï	21	33	51	8	Sequence 47, Appl
US-10-364-743-97	US-10-452-593-97	US-09-828-708-24	US-10-630-009-24	9 US-09-828-708-10	US-10-630-009-10	US-10-010-729-7	US-10-727-155-14	US-10-292-088-58	US-10-364-743-11	-36	US-10-452-593-11	US-10-452-593-99	9-880-748-169	0-293-418-1	ġ	6	US-10-384-060-46	ò	0-396-578-2	ò	0-396-578	10-396-578	US-10-844-424-36	10-844-42	10-844-42	Ŧ	-10-798-380-2	7	÷	-11-074-	-11-074-	US-11-074-803-81	-10-269-
12	16	o	17	Φ	17	14	17	15	15	15	16	16	10	15	15	10	15	15	16	16	16	16	16	16	16	16	16	11	20	20	20	20	15
135	135	17	17	101	101	119	123	125	137	137	137	137	252	252	470	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	41
7.76	7.76	95.5	95.5	95.5	95.5	95.5	94.3	94.3	94.3	94.3	94.3	94.3	94.3	94.3	94.3	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2		93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2
98	98	84	84	84	84	84	83	83	83	83	83	83	83	83	83	82	82	82	82	82	82	85	85	82	82	82	82	82	82	85	82	82	82
12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	. 31	32	33	34	32	36	37	38	39	40	41	42	43	44	4.5

ALIGNMENTS

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Gaps
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Sequence 300, Application US/10989462

Sequence 300, Application US/10989462

Publication No. US20050220795A1

GENERAL INFORMATION:

APPLICANT: Wittrup, K. Dane

APPLICANT: Wittrup, K. Dane

APPLICANT: Wittrup, X. Dane

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 01997-329001

CURRENT FILING DATE: 2004-11-15

PRIOR PILING DATE: 2004-11-15

PRIOR PILING DATE: 2004-01-19

PRIOR FILING DATE: 2004-01-19

PRIOR FILING DATE: 2004-04-19

NUMBER: OF 500 10 NOS: 319

SOFTWARE: FBSEESEQ for Windows Version 4.0

LENGTH: 17

LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

98.9%; Score 87; DB 18; Length 17;
Best Local Similarity 94.1%; Pred, No. 1.6e-06;
Matches 16; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetically generated peptide US-10-989-462-300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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1 IISYDGSKKYYADSVKG 17

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US-09-880-748-916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 914, Application US/09880748

Sequence 914, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:
TILE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPERENCE: PF523
CURRENT FILING DATE: 2001-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2001-01-17

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

Best Local Similarity 94.1%; Pred. No. 1.2e-05;
Matches 16; Conservative 1; Mismatches 0; Indels
     Sequence 262, Application US/10989462

Sublication No. US20050220795A1

GENERAL INFORMATION:
APPLICANT: Wittrup.
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 01997-329001
CURRENT APLICATION NUMBER: US/10/989,462
CURRENT PLING DATE: 2004-11-15
PRIOR PLING DATE: 2004-11-14
PRIOR PLING DATE: 2003-11-4
SPRIOR PLING DATE: 2003-11-4
SPRIOR PLING DATE: 2003-11-4
SPRIOR PLING DATE: 2003-11-14
SPRIOR PLING DATE: 2003-11-14
SPRIOR PLING DATE: 2003-11-14
SPRIOR PLING DATE: 2003-11-14
SPRIOR PLING DATE: 2003-11-15
SOFTWARE: PEASEGO for Windows Version 4.0
SSEQ ID NO 262
LENGTH: 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Synthetically generated peptide
US-10-989-462-262
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CORGANISM: Homo sapiens
US-09-880-748-914
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Best Local Similarity
Matches 16; Conserv
US-10-989-462-262
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; Publication No. US20030059937A1
; GENERAL INFORMATION:
    APPLICANT; Ruben et al.
    TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
    TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
    TITLE REFERENCE: PF523
    CURRENT FILING DATE: 2001-66-15
    PRIOR PILING DATE: 2000-06-15
    PRIOR PILING DATE: 2000-06-15
    PRIOR FILING DATE: 2000-10-17
    PRIOR FILING DATE: 2000-10-17
    PRIOR FILING DATE: 2001-03-16
    PRIOR FILING DATE: 2001-03-16
    PRIOR FILING DATE: 2001-03-16
    PRIOR FILING DATE: 2001-03-21
    PRIOR PILING DATE: 2001-03-21
    PRIOR FILING DATE: 2001-05-25
    NUMBER OF SEQ ID NOS: 2239
    SOFTWARE: Patentin Ver. 2.0
    SEQ ID NO:25: 2239
    SEQ ID NO:25: 229
US-09-880-748-916

Sequence 916, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF23

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2000-66-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

NUMBER: OF SEQ ID NOS: 3239

SOFTWARE: PATCHTIN VET. 2.0

SEQ ID NO 916

LENGTH: 248
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98.9%; Score 87; DB 10; Length 248;
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels
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98.9%; Score 87; DB 10; Length 248;
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels
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CORGANISM: Homo sapiens
US-09-880-748-1323
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; ORGANISM: Homo sapiens
US-10-293-418-916
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; ORGANISM: Homo sapiens
US-10-293-418-1323
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US-10-293-418-1323
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                                                                                 Sequence 914, Application US/10293418

Publication No. US20030223996A1

GENERAL INPORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REPRENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

FRIOR PILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR FILING DATE: 2000-03-16

PRIOR FILING DATE: 2000-03-16

PRIOR FILING DATE: 2000-06-16

PRIOR FILING DATE: 2000-06-16
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i Sequence 916, Application US/10293418

i Publication No. US20030223996A1

i CENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

FILE REFERENCE: 2002-11-27

PRIOR PLING DATE: 2001-11-16

PRIOR PLING DATE: 2001-11-16

PRIOR PLING DATE: 2001-12-19

PRIOR PLING DATE: 2001-06-15

PRIOR PLING DATE: 2001-06-15

PRIOR PLING DATE: 2001-06-25

PRIOR PLING DATE: 2001-05-25

PRIOR PLING DATE: 2001-05-25

PRIOR PLING DATE: 2001-05-31

PRIOR PLING DATE: 2001-03-11

PRIOR PLING DATE: 2001-03-11

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2000-06-16

PRIOR PLING DATE: 2000-06-16
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CORGANISM: Homo sapiens
US-10-293-418-914
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| Quaery Watch | Machael | 26.34, Score 87; DB 15; Length 248; | | |
| Matches | 15; Conservative | 17; Mismatchem 0; Indels 0; Gaps 0; |
| Oy | 11; STOSSKYYMBSWG | 16; | Mismatchem 0; | Indels 0; Gaps 0; |
| Db | 50 VISTOSSKYYMBSWG | 17; | Mismatchem 0; | Indels 0; | Indel
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Gaps

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Query Match 97.7%; Score 86; DB 15; Length 135; Best Local Similarity 94.1%; Pred. No. 1.9e-05; Matches 16; Conservative 1; Mismatches 0; Indels
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APPLICANT: Frederickson, Shana
APPLICANT: Wild, Martha A.
APPLICANT: Wild, Martha A.
APPLICANT: Wolan, Mary Jean
TITLE OF INVENTION: IMMUNTHERAPEUTICS FOR BIODEFENSE
FILE REPERRING: 98 CIP (1087-73 CIP)
CURRENT APPLICATION NUMBER: US/10/452,593
CURRENT FILING DATE: 2003-06-02
PRIOR FILING DATE: 2003-06-02
PRIOR FILING DATE: 2003-02-11
PRIOR FILING DATE: 2003-02-11
PRIOR FILING DATE: 2002-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Brederickson, Shana
APPLICANT: Frederickson, Shana
APPLICANT: Wild, Martha Martha
APPLICANT: Wild, Martha
APPLICANT: Wo. US20040009178Alan, Mary Jean
TITLE OF INVENTION: IMMUNTHERAPEUTICS FOR BIODEFENSE
FILE REFERENCE: 84 (1087-73)
CURRENT APPLICATION NUMBER: US/10/364,743
CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 60/428,807
PRIOR PILING DATE: 2002-11-25
                                                                                                                                                                                                                                                  , OTHER INFORMATION: Synthetically generated peptide US-10-989-462-276
                                                                      NUMBER OF SEQ ID NOS: 319
SOFTWARE: RESURED for Windows Version 4.0
SEQ ID NO 276
LENGTH: 252
                       60/563,514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 97, Application US/10364743; Publication No. US20040009178A1; GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.2
SEQ ID NO 97
LENGTH: 135
                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 2004-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: human
US-10-364-743-97
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GENERAL INVUMENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF52322
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR PLILING DATE: 2001-11-16
PRIOR PLILING DATE: 2001-12-19
PRIOR PLILING DATE: 2001-06-15
PRIOR PLILING DATE: 2001-06-15
PRIOR PLILING DATE: 2001-06-15
PRIOR PLILING DATE: 2001-06-25
PRIOR PLILING DATE: 2001-03-21
PRIOR PLILING DATE: 2001-03-16
PRIOR PLILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247

SEQ ID NO 1114

LENGTH: 251
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                                                                                                                                                                                                                              Query Match

98.9%; Score 87; DB 10; Length 251;
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels
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Sequence 276, Application US/10989462

Sequence 276, Application US/10989462

BENERAL INFORMATION:
THIRD OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION: THEREOF

FILE REFERENCE: 01997-329001

CURRENT FILING BATE: 2004-11-15

PRIOR APPLICATION NUMBER: US 60/520,114
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98.9%; Score 87; DB 15; I
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1114, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1114
LENGTH: 251
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CORGANISM: Homo sapiens
US-10-293-418-1114
                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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US-10-293-418-1114
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RESULT 11

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PRIOR APPLICATION NUMBER: US 60/376,408
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 60/428,807
PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VEXBION 3.2
LENGTH: 135
                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: human
US-10-452-593-97
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ö Score 86; DB 16; Length 135; Pred. No. 1.9e-05; 1; Mismatches 0; Indels Query Match
Best Local Similarity 94.1%;
Matches 16; Conservative

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RESULT 14

US-09-828-708-24

i Sequence 24, Application US/09828708

i Patent No. US20020146753A1

i GENERAL INFORMATION:

A APPLICANT: Butron, D.

A APPLICANT: Schaller, M.

ITILE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici

ITILE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici

TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase

ITILE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase

CURRENT APPLICATION NUMBER: US/09/828,708

CURRENT PILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 24

LENGTH: 17

TYPE: PRT

ORGANISM: Homo sapiens

US-09-828-708-24
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Gaps ó Length 17; Query Match 95.5%; Score 84; DB 9; I Best Local Similarity 88.2%; Pred. No. 4.7e-06; Matches 15; Conservative 2; Mismatches 0; 1 IISYDGSKKYYADSVKG 17 ò

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RESULT 15
US-10-630-009-24
; Sequence 24, Application US/10630009
; Publication No. US20050080239A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Button, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autcantibodies to glucose-6-phosphate isomerase and their partici;
; TITLE OF INVENTION: Autcantibodies to glucose-6-phosphate isomerase and their partici;
; TITLE OF INVENTION: Autcantibodies to glucose-6-phosphate;
; TITLE OF INVENTION: Autcantibodies to glucose-6-phosphate;
; FILE REFERENCE: 1341.065052
; CURRENT APPLICATION NUMBER: US/10/630,009
; PRIOR PILING DATE: 2001-04-06
; NUMBER: OF SEQ ID NOS: 123
; SOFTWARE: PASTES of or Windows Version 4.0
; SEQ ID NO 24
LENGTH: 17
; TYPE: PRI
; ORGANISM: Homo sapiens
US-10-630-09-24

Gaps ö Length 17; Query Match
Best Local Similarity 88.2%; Pred. No. 4.7e-06;
Matches 15; Conservative 2; Mismatches 0

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Search completed: October 14, 2005, 17:00:42 Job time : 121.859 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

October 14, 2005, 16:02:59 ; Search time 23.6406 Seconds (without alignments) 69.190 Million cell updates/sec Run on:

US-10-614-959-11 88 1 IISYDGSKKYYADSVKG 17 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	heavy chain V-	heavy chain V	heavy	heavy chain V	heavy chain V	heavy chain V	heavy chain V	heavy	heavy chain -:	heavy chain V	heavy chain V	heavy chain V	heavy chain V	heavy chain -	heavy chain V	heavy	heavy chain V	heavy chain V	heavy	heavy chain -	heavy chain -	heavy chain pr	heavy chain v	cha					
SUMMARIES	ID	PL0120	844115	PL0116	S29546	PH1646	PH1644	PH1643	PH1645	S38490	846390	S46392	S36270	S31677	S31116	F36005	531112	\$19666	G36005	E36005	831119	S38493	PL0098	S31603	S31679	S31674	S31701	PH1642	S46391	_
	DB											~																		
	Length	94	97	98	98	109	109	11	111	113	114	114	117	118	118	119	120	121	121	122	122	123	130	132	134	139	137	108	114	119
مد	Ouery Match		÷	ë	ë.	ω.	ë.	<u>.</u>	'n.	ë.	'n.	93.2	ë.	٠.	ë.	ë.	÷	ς.	Ä.	÷	<u>.</u>	÷.	ë.	<u>.</u>	<u>.</u>	۳.	ζ.			
	Score		82	82	82	82	82	82	82	82	82	82	82	82	85	82	82	82	82	85	85	85	82	82	82	82	77	75	75	75
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heavy chain	heavy chain heavy chain heavy chain heavy chain	heavy heavy heavy		Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r
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			4.67	
30	, w w w	38	444	4 4 4 4 4 0

ALIGNMENTS

Takeny Canalin V-111 region (TD-VO) - numan (Eragment) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: D7-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004 C.Spacession: PL0120 R.Sibird, J.; Gallii, N.; Link, M.; Stites, D.; Sklar, J. J. Exp. Med. 168, 229-245, 1988 A.Fitle: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin A.Reference number: PL0116; MUID:88286083; PMID:2840480 A.FReference number: PL0116; MUID:88286083; PMID:2840480 A.FReference number: PL0120 A.Molecule type: mRNA A.Residues: 1-94 effIRA A.FReferences: UNIPROT:08WUK1; UNIPROT:09UL33 A.Experimental source: B cells from patient TD with acute lymphoblastic leukemia; hamunoglobulin homology C.Superfamily: immunoglobulin V region; fimunoglobulin homology C.Superfamily: immunoglobulin V region; fimunoglobulin homology C.Steywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin F.31-35/Region: complementarity-determining 1 F.49-65/Region: complementarity-determining 2 Cuery Match Best Local Similarity 88.2%; Pred. No. 7.2e-06; Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0; IISYDGSKIXYXADSVKG 17 C. IIIII

50 VISYDGSNKYYADSVKG 66 g

RESULT 2
S44115
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #text_change 24-May-2001
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Date: 13-Jan-1995 #sequence_revision: S44115
R;Hawkins: R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable relateres: S44115
A;Accession: S44115
A;Status: preliminary
A;Anolecule type: DNA
A;Residues: 1-97 - 4NA
A;Residues: 1-97 - 4NA
A;Residues: 1-97 - 4NA
A;Cross-references: EMBL:Z31384; NID:g472969; PIDN:CAA83259.1; PID:g940526
C;Superfamily: immunoglobulin
C;Keywords: heterotetramer; immunoglobulin

Gaps ö Query Match 93.2%; Score 82; DB 2; Length 97; Best Local Similarity 88.2%; Pred. No. 7.5e-06; Matches 15; Conservative 1; Mismatches 1; Indels

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Til heavy chain V region (clone 6H7) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Dacte: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: PH1643
R;Hilbon, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Fitle: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc A;Reference number: PH1642; MUID:93301610; PMID:8315388
                                                                                                                                                                                                                                                                                Ig heavy chain V region (clone 6H12) - human (fragment)
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Species: 24-Reb-1994 #sequence_revision 24-Reb-1994 #text_change 09-Jul-2004
C;Accesion: PH1646
C;Accesion: PH1646
A;Accesion: PH1641
A;Accesion: PH1642; MUID: 93301610; PMID: 9315388
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc
A;Accesion: PH1642; MUID: 93301610; PMID: 9315388
A;Accesion: PH1644
A;Accesion: PH1644
A;Accesion: PH1644
A;Accesion: PH1644
A;Accesion: MIPROT: OWNUKI
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Superfamily: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ig heavy chain V region (clone 5D11) - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Atter 2, Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C; Atcession: PH1644
R; Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-36, 1993
A; Fitle: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylocal A; Reference number: PH1642; MUID:93301610; PMID:9315388
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
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Pred. No. 8.4e-06;
1; Mismatches 1; Indels
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Pred. No. 8.4e-06;
1; Mismatches 1; Indels
                                 Indels
      88.2%; Pred. No. 7.5e-06;
ive 1; Mismatches 1;
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15; Conservative
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Best Local Similarity 88.2.
Best Local Similarity
Best. 15; Conservative
                                 15; Conservative
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Best Local Similarity
Best Local Similarity
Matches 15; Conserv
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A; Residues: 1-109 <HIL>
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                                                                                                                                                                                                          Ig heavy chain V-III region (AW-Vx) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: PLO116; S26892
R;Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 169, 229-245, 1988
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin A;Reference number: PLO116; MUID:88286083; PMID:2840480
A;Accession: PLO116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Molecule type: DNA
A, Residues: 1-98 <TOM>
A, Residues: 1-98 <TOM>
A, Residues: 1-98 <TOM>
A, Cross-references: EMBL: Z17394; NID: g32843; PIDN: CAA78997.1; PID: g32844
A, Note: designated COS-8
A, Note: designated COS-8
B, Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A, Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A, Reference number: S26885; MUID: 93021117; PMID: 1404388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mENA
A; Residues: 1-98 cBIR>
A; Residues: 1-99 cBIR>
A; Experimental Bource: B cells from patient AW with acute lymphoblastic leukemia, ALL
A; Note: the sequence shows the V region (AW-Vx) from a nonproductive DNA rearrangement
A; Note: the sequence shows the V region (AW-Vx) from a nonproductive DNA rearrangement
B; Tomlinson, I.M.; Walter, G; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A; Mol. Biol. 227, 776-798, 1992
A; Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A; Reference number: $26885; MUID:93021117; PMID:1404388
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Ig heavy chain V region (COS-8 / DP-46) - human (fragment)
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S29546; S2688
R;Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A;Reference number: S29546
A;Accession: S29546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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A;Note: designated DP-46
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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88.2%; Pred. No. 7.5e-06;
tive 1; Mismatches 1;
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                     1 IISYDGSKKYYADSVKG 17
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Matches 15; Conservative
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-98 <TO2>
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A; Residues: 1-98 <TOM>
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Gistory chain V region (clone alpha-TNF-E1) - human (fragment)
Cispecies: Homo sapiens (man)
Cispecies: Siscon (man)
Riciffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: Siscon (min)
A;Reference number: Siscon (min)
A;Reference number: Siscon (min)
A;Reference number: Siscon (min)
A;Residues: 1-17 cGRI>
A;Cross-references: EMBL: ZisB39; NID:933118; PIDN:CAA79291.1; PID:9939898
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology cIMM>
   Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46390
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
A;Ticle: In virto assembly of repertoires of antibody chains on the surface of phage by J;Reference number: S46390
A;Reference number: S46390
A;Reference number: S46390
A;Reference number: S46390
A;Recension: S46390
A;Residues preliminary
A;Moceule type: DNA
A;Residues: 1-114 <FIG.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain V region (VH-28) - human
CjSpecies: Homo Bapiens (man)
CjAccession: 846392
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by sherence number: 846390; MUID:94284092; PMID:8196048
A;Accession: 846392
A;Accession: S46392
A;Accession: S46393
A;Accession: Stellanary
A;Accession: Stellanary
A;Accession: Stellanary
A;Cross-references: EMBL:231688; NID:9499306; PIDN:CAA83493.1; PID:gl335145
C;Superfeamly: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 88.2
Matches 15; Conservative
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Matches 15; Conservative
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S46392
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S36270
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PH1645
Ig heavy chain V region (clone 6C8) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: PH1645
R;Hillson, U.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Fitle: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylc
A;Reference number: PH1642; MUID:93301610; PMID:8315388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: 838490
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a page.
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A,Residues: 1-13 < MAR>
A,Residues: 1-13 < MAR>
C,Superfamily: 1mmunoglobulin V region; immunoglobulin homology
C,Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
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A;Molecule type: mRNA
A;Residues: 1-111 <HIL>
A;Residues: 1-111 <HIL>
A;Cross-references: UNIPROT: OSWUK1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-111 < HIL>
A; Residues: 1-111 < HIL>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterocetramer; immunoglobulin
F; 7-90/Domain: immunoglobulin homology < IMM>
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88.2%; Pred. No. 8.7e-06;
iive 1; Mismatches 1; Indels
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ilarity 88.2%; Pred. No. 8.6e-06;
Conservative 1; Mismatches 1; Indels
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88.2%; Pred. No. 8.6e-06;
tive 1; Mismatches 1; Indels
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A,Accession: S38490
A,Status: preliminary
A,Molecule type: DNA
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Best Loca Matches

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Length 119 1; Indels

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A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene f
A;Reference number: A36005; MUD:90349571; PMID:2117273
A;Accession: F36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residus: 1-119 <SCH>
A;Cross-references: UNIPROT:QWUKI; GB:M34026
C;Genetics: 1-119 <SCH>
A;Cross-references: GDB:118731; OMIM:146910
A;Gene: GDB:IGM31,314q22.33
A;Cross-references: GDB:118731; OMIM:146910
C;Genetics: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IVM>
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88.2%; Pred. No. 9.2e-06;
tive 1; Mismatches 1;
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R. Raaphorst, F. M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992
A. Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A; Reference number: S31104; MUID:92111633; PMID:1730252
A, Accession: S31116
A, Residue: preliminary; nucleic acid sequence not shown; translation not shown
A, Molecule type: mRNA
A, Residues: 1-118 cRA>
A, Residues: 1-118 cRA>
A, Cosserences: UNIPROT:08WUK1; EMBL:X62966
A, October: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C, Superfamily: immunoglobulin v region; immunoglobulin homology
C, Superfamily: immunoglobulin homology < IMM>
F,15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31677 #sequence revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31677 #sequence revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31677 #sequence L: Boubli, L: Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
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C;Species: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
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A,Status: preliminary
A;Status: preliminary
A;Residues: preliminary
A;Residues: L118 «CUI»
A,Residues: L118 «CUI»
C,Stoperferally: immunoglobulin v region; immunoglobulin homology
C,Superfemily: immunoglobulin immunoglobulin homology
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88.2%; Pred. No. 9e-06;
iive 1; Mismatches 1; Indels
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tive 1; Mismatches 1;
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Pred. No. 9.1e-06;
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Ig heavy chain V region - human (fragment)
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QGmzq6 QGgmx2 Q001063 Q05218 Q069218 Q099171 Q099171 Q098003 Q01094 Q01094 Q01094

Q6IN78 Q6MZQ6 Q6GMZQ Q6GMZQ Q920E7 Q65ZL8 Q66ZXL8 Q6GPX4 Q9G771 Q9G77 HV57 MOUSE HV57 MOUSE HV57 MOUSE XC81 METJA

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homo sapien
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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PIR; PH1642; PH1642.

R PIR; PH1643; PH1643.

R PIR; PH1643; PH1643.

R PIR; PH1645; PH1645.

R PIR; PH1645; PH1646.

DR PIR; PL0120; PL0120.

DR PIR; S31119; S31119.

DR PIR; S30442; S70442.

DR PRS; P01861; 1A04.

DR PGam; PP07664; C1-8et; 4.

DR PROSITE; PS00290; IG MHC; UNKNOWN 3.

DR PROSITE; PS00290; IG MHC; UNKNOWN 3.

PROSITE; PS00290; IG MHC; UNKNOWN 3.

PROSITE; PS00290; IG MHC; INKE; 5.

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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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Best Local Similarity 87.5%; Pred. No. 0.00022;
Matches 14; Conservative 0; Mismatches 2; Indels
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93.2%; Score 82; DB 2; Length 613;
Best Local Similarity 88.2%; Pred. No. 6.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels
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Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035024; AAD56260.1; --
PIR, S78486; S78486.
HSSP; PO1772; ZFB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGV; 1.
PROSITE; PSS0835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 01, Created)
(Rel. 01, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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HV3G_HUMAN
ID HV3G HUMAN
AC P01768;
DT 21-JUL-1986 (1
DT 21-JUL-1986 (1
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NON_TER
SEQUENCE
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MEDINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Klausher R.D., Colling F.S., Wargner L., Shenmen C.M., Schuler G.D.,

Klausher R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Paramer A.A., Rubin G.M., Haieh F.,

Diatchenko L., Marusina K., Paramer A.A., Rubin G.M., Heleh F.,

Brapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S. Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Makealey R.W., Touchman J.W., Green E.D., Dickson M.C.,

Radriquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.2%; Score 82; DB 2; Length 240;
88.2%; Pred. No. 2.3e-05;
tive 1; Mismatches 1; Indels
                                                                                                                            MEDLINE=97362799; PubMed=9219263;

Kontermann R.E., Wing M.G., Winter G.;

Complement recruitment using bispecific diabodies.";

Nat. Biotechnol. 15:629-631(1997).

EMBL; X13056; CAA73499.1;

InterPro; IPR00359; Ig.

InterPro; IPR003199; Ig.

InterPro; IPR003596; Ig.v.

Remain Should Shou
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; F36005; R36005.
PIR; G36005; G36005.
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240 AA; 25569 MW; FDCFD3645F64B373 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      613 AA
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                           SEQUENCE FROM N.A. STRAIN=Clq/7;
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                        NCBI_TaxID=9606;
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2 To:39:19 2005
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SEQUENCE.

W ADLINE=81013859; PubMed=6774332;

WABLINE=81013859; PubMed=6774332;

WABLINE=81013859; PubMed=6774332;

WABLINE=81013859; PubMed=6774332;

Tocation of a possible JH segment.";

Tocation of a possible JH segment.";

Tocation of a possible JH segment.";

Proc. Natl. Acad. Sci. U.S.A. 77:329-3343(1980).

C -I - MISCELLANEOUS: This mu chain was isolated from the plasma of a patient with macroglobulinemia.

C -I - MISCELLANEOUS: This mu chain was isolated from the plasma of a patient with macroglobulinemia.

PREP. POTO: 2.PH. Contains 1 immunoglobulin-like domain.

PREP. POTO: 2.PH. Contains 1 immunoglobulin-like domain.

PREP. POTO: 2.PH. Contains 1 immunoglobulin-like domain.

PREP. POTO: 2.PH. Contains 1 immunoglobulin N.S.

SO: GO:000555; P:immune response; NAS.

InterPro: IPRO0310; Ig-1.

SMART; SMO0406; IG-V.

SMART; SMO0406; IG-V.

SMART; SMO0406; IG-V.

SMART; SMO0406; IG-V.

PRES. PRES. PRES. IG LIKE; 1.

PROSITE; PRES. IL LIKE; 1.

PROMATN.

TOTALLANEOUS.
                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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        DOMAIN
        1
        112
        19-like.

        MOD_RES
        1
        1
        Pyrrolidone carboxylic aci

        NON_TER
        122
        122
        SEQÜENCE
        122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

              05-JUL-2004 (Rel. 44, Last annotation update) Ig heavy chain V-III region CAM. Homo sapiens (Human).
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Query Match
84.1%; Score 74; DB 1; Length 122;
Best Local Similarity 70.6%; Pred. No. 0.00024;
Matches 12; Conservative 3; Mismatches 2; Indels 1 IISYDGSKKYYADSVKG 17 ď ઠે

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:|||:| ||||:|||| 50 VISYBGBBKYYABSVKG 66

417 AA

PRT;

06N093; 05-JUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Hypochetical protein DKF2p686104196 (Fragment). Name-DKF2p686104196; Homo sapiens (Human). PRELIMINARY; Q6N093

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606,

TISSUENCE FROM N.A.

TISSUE-Human esophagus tumor;

TISSUE-Human cDNA Consortium;

The German Human cDNA Consortium;

A mbutt R., Heubner D., Mewes H.W., Well B., Amid C., Osanger A.,

Robo G., Han M., Wiemann S.;

L. Submitted (ANG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BX640623; CAR45777.1; -..

RSPP: P01861; 1ADO.

InterPro; IPR003159; IG.

InterPro; IPR003159; IG.

InterPro; IPR003159; IG.

InterPro; IPR003159; IG.

InterPro; IPR003106; IG.

InterPro; IPR003106; IG.

R InterPro; IPR003106; IG.

R REART; SM00409; IG; 2.

SWART; SM00400; IGc.;

SWART; SM00406; IGv; 1.

.; 0 Query Match 80.7%; Score 71; DB 2; Length 417; Best Local Similarity 70.6%; Pred. No. 0.0029; Matches 12; Conservative 4; Mismatches 1; Indels PROSITE; PSS0835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
NON_TER 1 1 1
SEQUENCE 417 AA; 46061 MW; C4518E844CFB883C CRC64; STKER

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OGBCN4 PRELIMINARY; PRT; 493 AA.

25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypotherical protein DKFZp686E23209 (Fragment).
Name=DKKZp686E23209;
Name=DKRZp686E23209;
Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TISSUERCE FROM N.A.

TISSUERCCTUM tumor;

TISSUERCCTUM tumor;

The German consortium;

Brocker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,

Osanger A., Fobo G., Han M., Wiemann S.;

Submitted (Audra-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; CR749861; CA418705-1;

R InterPro; IPR001599; IG.

R InterPro; IPR001509; IG.

R InterPro; IPR001506; Ig.—W.

R InterPro; IPR001506; Ig.—W.

R InterPro; IPR001506; Ig.—W.

R Fam; PF00654; C1-set; 3.

R Fam; PF00647; IG.;

R PR001715; SM00409; IG. 2.

SMART; SM00409; IG. 2.

SMART; SM00406; IG.; 1.

R PROSITE; PS00190; IG. MKC, UNKNOWN_2.

W PROSITE; PS00190; IG.—WIC.

W PR

493 AA; 54117 MW; A1E4F5ED3FA8AB40 CRC64; SEQUENCE

79.5%; Score 70; DB 2; Length 493; 70.6%; Pred. No. 0.0052; tive 4; Mismatches 1; Indels Query Match
Best Local Similarity 70.67
Matches 12; Conservative

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:|||:| |::||||||| 92 VISYEGGKQHYADSVKG 108 1 IISYDGSKKYYADSVKG 17

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Q9Y509 Q9Y509; 01-NOV-1999 (TrEMBLrel. 12, Cz 01-NOV-1999 (TrEMBLrel. 12, La 01-OCT-2003 (TrEMBLrel. 25, La VH3 procein (Fragment). RESULT 8 Q9Y509

Created) Last sequence update) Last annotation update)

PRT;

Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens (Human)

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 493;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FLJ90170.
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HSSP, P01772; 2FB4.
InterPro; IPR00710; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
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70.6%; Pred. No. 0.016;
tive 3; Mismatches
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Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                   MEDLINE-96071149; PubMed-7475288;
Cao J., Veeclo R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
Lichtenstein A.K., Berenson J.R.;
"A CDIO-positive subset of malignant cells is identified in multiple
"A CDIO-positive subset of malignant cells is of second in multiple
myeloma using PCR with patient-specific immunoglobulin gene primers.";
Luckemia 9:1948-1953 [1995].
EMBL; 880860; AAD14339.1; -...
HSSP; P01842: 1AQK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO: 0005887; C:integral to plasma membrane; NAS. GO; GO: 0005887; C:integral to plasma membrane; NAS. GO; GO: 0016066; P:cellular defense response (sensu Vertebrata); NAS. InterPro; IPR007110; Ig-like.
InterPro; IPR00356; Ig-v.
SMART; SM00406; IGV; I.
NON_TER: PSS0835; IG LIKE; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Human rectum tumor;
Blocker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Blocker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Subo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538118; CAD98026.1; -.
EMBL; BX538118; CAD98026.1; -.
InterPro; IPR00110; Ig-1ike.
InterPro; IPR003597; Ig-c1.
InterPro; IPR003596; Ig-d.
InterPro; IPR003596; Ig-MHC.
InterPro; IPR003596; Ig-MHC.
InterPro; IPR003596; Ig-MHC.
Fran; PR07654; CL-8et; 3.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.4%; Score 69; DB 2; Length 147; 76.5%; Pred. No. 0.002; ative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 482 AA; 52852 MW; EDA75F1901D1A034 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-071-2003 (TrEMBLrel. 25, Created)
01-071-2003 (TrEMBLrel. 25, Last sequence update)
Hypothettoal (TrEMBLrel. 26, Last annotation update)
Hypothettoal protein DKFZp686N02209.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 76.5
hes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                              SEQUENCE FROM N.A.
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                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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QBNCL6
ID QBNCL6
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Q7Z351

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RESULT 9

Matches

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                                                   / Match 15.0%; Score 66; DB 2; Length 122; Local Similarity 81.2%; Pred. No. 0.0053; nes 13; Conservative 1; Mismatches 2; Indels
122 122
122 AA; 13579 MW; 36054D41366545B8 CRC64;
                                                                                 Best Loca
Matches
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493 AA

PRT;

PRELIMINARY;

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2 ISYDGSKKYYADSVKG 17
          51 ISNDGSNKFYADSVKG 66
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-1986 (Rel. 44, Last annotation update)
IG heavy chain V-III region BUR.
IG heavy chain V-III region BUR.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 119 AA STANDARD; RESULT 12
HV3L HUMAN
AC P01773;
DT 21-JUL-1986
DT 21-JUL-1986
DT 21-JUL-1986
DT 21-JUL-1986
DT 21-JUL-1986
DT 21-JUL-1986
DT OS-JUL-2004
DE IG heavy chains
OC EURATYOTA;
RN MEDLINE=7915]
RA MEDLINE=7915]
RA MEDLINE=7915]
RA MEDLINE=7915]
RA MEDLINE=7915]
RA BEQUENCE (MYE
RY REQUENCE (MYE
RY BEQUENCE (MYE
RY BOLINE=7915)
RA GOIG GOOOO095
DR HSSP, PO1772
DR GOIG GOOOO095
DR HOSPER, PROOOF
DR PRAM; PROOOF
DR P

Pyrrolidone carboxylic acid 22 96 28 28 N-linked (GlcNAc. .). 119 119 119 AA; 12981 MW; 12A709A75344D024 CRC64;

/ Match 73.9%; Score 65; DB 1; Length 119; Local Similarity 70.6%; Pred. No. 0.0076; He 12; Conservative 2; Mismatches 3; Indels Query Match

1 IISYDGSKKYYADSVKG 17 Best Loca Matches

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RESULT 13

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01-MAY-2000 (TERMELREI. 13, Created)
01-MAY-2000 (TERMELREI. 13, Last sequence update)
01-MAY-2004 (TERMELREI. 26, Last annotation update)
Imunoglobulin heavy chain (Fragment).
Eukano sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. PRELIMINARY; O9ULB6 Q9ULB6 11D Q9 01D Q0 01D D1 011 01D D1 011 01D D2 011 01D D2 011 01D D2 011 01D D3 011 01D 01D 011 01D 01D 011 01D 011 01D 011 01D 011 01D 011 01D 011 01D 011

95 AA.

SEQUENCE FROM N.A.
Tange Y., Kayano H.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO35266; BAA87067.1; -.
PIR; PH0872; PH0872.

ö 72.7%; Score 64; DB 2; Length 95; 75.0%; Pred. No. 0.0087; tive 1; Mismatches 3; Indels PIR; \$36280; \$36280.
HSSP; P01820; 1G7J.
InterPro; IPR007110; 1g-like.
InterPro; IPR003596; 1g_v.
SMART; \$M00406; 1Gv; 1.
PROSITE; PS50835; 1G_LIKE; 1.
NON_TER 95 95
SEQÜENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64; Query Match 72.7%; Best Local Similarity 75.0%; Matches 12; Conservative

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PRT; STANDARD; RESULT 14 HV3H_HUMAN ID HV3H_HUMAN AC P01769;

21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
heavy chain V-III region GA.
Homo sapiens (Human). 122 AA

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606;

SEQUENCE

MEDLINE=74175307; PubMed=4208843;
Florent G., Lehman D., Putnam F.W.;
"The switch point in mu heavy chains of human IgM immunoglobulins.";
Blochemistry 13:2482-2488(1974).
-!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's

Ig-like. Pyrrolidone carboxylic acid. 122 122 122 AA; 13166 MW; 74E5B6959E84100A CRC64; FEAN, PEONOAT, 197.

SMART, SMO0406, IGV, 1.

DROSITE, PSS035, IG_LIKE; 1.

Driect protein sequencing; Immunoglobulin V region;

Pyrrolidone carboxylic acid.

DOMAIN

1 112

NOD_RES

1 1 Pyrrolidone carboxylic

NON_TER 122

SEQÜENCE 122 AA, 13166 MW; 74ESB6959E84100A CRCE

72.7%; Score 64; DB 1; Length 122; 64.7%; Pred. No. 0.011; tive 3; Mismatches 3; Indele 11; Conservative Local Similarity

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:|||:| :||| 50 VISYBGBBZYYAASVKG 66 1 IISYDGSKKYYADSVKG 17

PRELIMINARY; O6PJA4 O6PJA4 ID O6 AC O6 DT O5 DT 05

RESULT 15

Last sequence update) Last annotation update) Created) (TrEMBLrel. 27, C (TrEMBLrel. 27, L (TrEMBLrel. 27, L O6PJA4; 05-JUL-2004 (05-JUL-2004 (05-JUL-2004 (

Mon Dec

Hypothetical protein.

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TISSUE=Primary B-Cells;

XT TISSUE=Primary B-Cells;

XT TISSUE=Primary B-Cells;

XT TISSUE=Primary B-Cells;

XT Araubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XT Alaubberg R.L., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XT Alaushar R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Jodin T.B., Toshlyuki S., Carninol P., Prange C.,

Raps S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robers S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

XI Chards S., Worlley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XI Chards S., Worlley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XI Chards J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

XI Barbeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Alakeley R.W., Touchman J.W., Green E.D., Myers R.W., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,

Alakeley R.W., Touchman J.W., Green E.D., Myers R.W.,

Johns S.J., Marra M.A.;

Johns S.J., Marra M.A.;

Tand mouse cDNA sequences.",

R. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
               Homo Gapieng (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.7%; Score 64; DB 2; Length 470; 75.0%; Pred. No. 0.05; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.; Submitted (DRC-2001) to the EMBL/GenBank/DDBJ databases. Submitted (DRC-2001) to the EMBL/GenBank/DDBJ databases. BMB.; BCO18747; AAH18747.1; -. HSSP; P01861; IADQ. InterPro; IPR0031599; Ig. InterPro; IPR00110; Ig-11ke. InterPro; IPR001597; Ig_c1. InterPro; IPR003106; Ig_wr. InterPro; IPR003506; Ig_wr. InterPro; IPR003596; Ig_w. PF07654; Cl-8et; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 470 AA; 51715 MW; 7B49556AllFD7D99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 3.
PROSITE; PSS0835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                                                                           SEQUENCE FROM N.A.
                                                                Mammalia; Eutheri
NCBI_TaxID=9606;
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2 ISYDGSKKYYADSVKG 17 ઠે

Local Similarity 75.0 nes 12; Conservative

Best Loca Matches

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Gaps

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Search completed: October 14, 2005, 16:19:51 Job time : 115.156 secs

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GenCore version 5.1.6
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October 14, 2005, 15:51:19; Search time 84.5625 Seconds (without alignments) 50.310 Million cell updates/sec Run on:

US-10-614-959-12 50 1 ASIAAARVLDY 11 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2003bs:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	lon	Anti-fact	Anti-fact	Oil-aggor	Human nol	Bacterial	Bacterial	Bacterial	Bacterial	Listeria	Zea mava	Zea maya	Amino aci	Bacterial	Arabidone	Arabidona	Seminary	Amino ari	Thermitas	Thermitas	Thermitas	Thermitas	Thermitae	Thormited	Thomasha	THE THIT CAB	Thermitas
	Description	Aav79070	Aav79077	Adi48827	Aao13448	Ad826132	Ad825655	Ad825373	Ad822602	Abb48560	Aaq18510	Aag18509	Aav37904	Ad928058	A8920306	Aag51887	AADRORSO	Aan80274	Aar54838	Aaw00768	Aaw00769	Aaw00774	Aaw00798	Apw00770	0.00me4	C/ /OMBO	Aaw00780
		AAY79070	AAY79077	ADJ48827	AA013448	ADS26132	ADS25655	ADS25373	ADS22602	ABB48560	AAG18510	AAG18509	AAY37904	ADS28058	AAG20306	AAG51887	AAP80850	AAP80274	AAR54838	AAW00768	AAW00769	PAW00774	PAW00798	AAW00770	AAW00775		MAWUU / 80
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de	Query Match	100.0	92.0	74.0	72.0	72.0	72.0	72.0	72.0	70.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	0	
	Score	20	46	37	36	36	36	36	36	35	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	7.0	5
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AAW00783 AAW00772 AAW00772 AAW00794 AAW00794 AAW00794 AAW00799 AAW00789 AAW00789 AAW00789 AAW00707 AAW00707 AAW00707 AAW00707	AAWOOBOO
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## ALIGNMENTS

AAY79070 standard; peptide; 11 AA.

(first entry) 12-JUN-2000

Anti-factor IX/IXa antibody H chain V domain CDR3 amino acid sequence

Complementarity determining region 3; CDR3; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CBBG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC.

Homo sapiens.

WO200012562-A1.

09-MAR-2000

99WO-US019453. 26-AUG-1999;

98US-0098233P. 99US-0122767P. 28-AUG-1998; 03-MAR-1999;

(GETH ) GENENTECH INC

Kirchhofer D; Judice JK, Навв РЕ, Devaux B, Eaton DL, Adams CW, Suggett S;

VPI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

Claim 2; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 3 (CDR3) of the heavy chain variable domain of a human anti-factor IX/Ixa Gla domain antibody. Factor IXA/Ixa dramin K dependent plasma serine procease that participates in the blood coagulation pathways. The Gla domain of factor IXA and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial 

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This sequence represents a complementarity determining region 3 (CDR3) of the heavy chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXa is a vitamin K dependent plasma serine protease that participates in the blood coagulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial cells and platelets. Compositions comprising the antibodies are used for the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is
the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary articy bypass graft (CABG), percutaneous transluminal coronary inflammation, septic shock, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complementarity determining region 3; CDR3; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-factor IX/IXa antibody H chain V domain CDR3 amino acid sequence
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kirchhofer D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.
                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                              Length 11;
                                                                                                                                                                                                                                                              100.0%; Score 50; DB 3; Length 11
100.0%; Pred. No. 0.003;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Judice JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hass PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY79077 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eaton DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Fig 2; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0098233P.
99US-0122767P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                        11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    Devaux B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-256595/22.
                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200012562-A1.
                                                                                                                                                                                                                              Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suggett S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams CW,
                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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The invention relates to a recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene. The construct is useful for transgent plant seed which has in its genome the construct, that is functional in the plant to transcribe the oil associated gene. The transgenic plant seed grows into a plant having enhanced seed oil as compared to wild type. The construct is useful for producing hybrid maize seed. The transgenic plant seed is useful for producing vegetable oil. The present sequence represents the amino acid sequence of an oil-associated gene related protein.
                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene for producing transgenic plant seed.
indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary angioplasty (PTCA), stroke, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
                                                                                                                                                                                     GapB
                                                                                                                                                                                                                                                                                                                                                                                                                                        oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 8; Length 408;
62;
                                                                                                                                                        Length 11;
                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ledeaux JR,
                                                                                                                                                        Score 46; DB 3;
Pred. No. 0.019;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               Oil-associated gene related protein #327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; SEQ ID NO 831; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Savage T,
                                                                                                                                                                                                                                                                                                                         ADJ48827 standard; protein; 408 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAR-2002; 2002US-0365301P.
26-JUN-2002; 2002US-0391786P.
26-JUN-2002; 2002US-0392018P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAR-2003; 2003US-00389566
                                                                                                                                                         92.0%;
                                                                                                                                                                                                                                                                                                                                                                                   06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laurie CC, Ravanello M,
                                                                                                                                                                                        10; Conservative
                                                                                                                                                                                                                    1 ASIAAARVLDY 11
                                                                                                                                                                                                                                               1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAURIE C C.
RAVANELLO M.
SAVAGE T.
LEDEAUX J R.
                                                                                                                                                                                                                                                1 ASIAAGRVLDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-142683/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROGERS J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 408 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2004025202-A1
                                                                                                                               Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                        ADJ48827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAUR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RAVA/)
(SAVA/)
(LEDE/)
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                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                             RESULT 3
ADJ48827
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          888888888888
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Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

Bacterial polypeptide #15165.

(first entry)

02-DEC-2004

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, call proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                   Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tisaue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID NO 27340; 1399pp + Sequence Listing; English
   IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.0%; Score 36; DB 4; Length 58; 70.0%; Pred. No. 12; 1; Indels tive 2; Mismatches 1; Indels
   ;
   Mismatches
                                                                                               AA013448 standard; protein; 58 AA.
                                                                                                                                                                Human polypeptide SEQ'ID NO 27340.
   ä
                                                                                                                                                                                                                                                                                                                                                                                     Fang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                         26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                              28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409.
                                                                                                                                         (first entry)
 8; Conservative
                                   ||:|||| ||
275 ASLAAARALD 284
                      1 ASIAAARVLD 10
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAI93379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 58 AA;
                                                                                                                                                                                                                                                             WO200164835-A2.
                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                          06-NOV-2001
                                                                                                                                                                                                                                                                                    07-SEP-2001
                                                                                                                    AA013448;
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Matches
                                                                         RESULT 4
AAO13448
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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Goldman BS;

Chen X,

Cao Y, Hinkle GJ, Slater SC,

WPI; 2004-061375/06.

(CAOY/) CAO Y.
(HINK/) HINKLE G J.
(SLAT/) SLATER S C.
(CHEN/) CHEN X.
(GOLD/) GOLDMAN B S.

20-FEB-2003, 2003US-00369493. 21-FEB-2002; 2002US-0360039P.

US2003233675-A1.

.8-DEC-2003.

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant cuch as maize or soybean. The method of producing a plant with the cerombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties.

CC The recombinant DNA construct is useful for improving plants with the cip properties or polynucleotide is useful for improving plant properties.

CC The recombinant DNA construct is useful for improving plants with increased resistance to plant disease, better growth rate by modification to content, improved yield by modified seed oil or protein yield and/or content, improved yield by modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, introgen or providing improved lignin production of carbohydrate, introgen or providing improved lignin production of carbohydrate, introgen or providing improved lignin production of carbohydrate, introgen or providing improved lignin provdering a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic form part of the printed specification but was obtained in electronic form was obtained.
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Claim 1; SEQ ID NO 15165; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Query Match
Best Local Similarity 63.00,
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RESULT 5 ADS26132 ID ADS26132 standard; protein; 652

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2 SIAAARVLDY 11 |:| ||||:| SVAQARVLEY

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Сарв

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Best Local Similarity 70.0 Matches 7; Conservative

Gaps

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Length 652

Score 36; DB 8; I Pred. No. 1.6e+02; 2; Mismatches 2;

72.0%;

Sequence 652 AA;

a

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|: |||| :||
255 AATAAARAIDY 265
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ADS25655 standard; protein; 652 AA Bacterial polypeptide #14688 (first entry) 02-DEC-2004 ADS25655 

Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oll yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

Bacteria.

US2003233675-A1.

18-DEC-2003

20-FEB-2003; 2003US-00369493

21-FEB-2002; 2002US-0360039P

(CAOY/) HINK/

HINKLE G J. SLATER S C. CHEN X (CHEN/) (SLAT/)

GOLDMAN B S.

Goldman BS Chen X, Slater SC, Hinkle GJ, Cao Y,

WPI; 2004-061375/06.

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 14688; 122pp; English.

WPI; 2004-061375/06

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polypoptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a cransformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant cauch as maize or soybean. The method of producing a transformed plant cauch an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polymucleotide or polypeptide is useful for improving plant properties. Cr. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or afcought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of carbohydrate, introgen or content, improved yield by modification of carbohydrate, introgen or phosphorus use and/or uptake, by modification of photosynthesis or by production, improved plant growth and development under at least one stress condition, improved lighin production or improved algant production or improved alganing inproved alganing production or improved alganing production or improved alganing production or improved second in the sequence data for this patent did not form part of the printed specification but was obtained in electronic form part of the printed specification but was obtained in electronic form part of the printed specification but was obtained in electronic content from uspro

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Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance, drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                        Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                         chen X,
                                                                                                       ADS25373 standard; protein; 655 AA.
                                                                                                                                                                                                                                                                                                                                                                                         Hinkle GJ, Slater SC,
                                                                                                                                                                                                                                                                                                    20-FEB-2003; 2003US-00369493.
                                                                                                                                                                                                                                                                                                                     21-FEB-2002; 2002US-0360039P.
                                                                                                                                                           Bacterial polypeptide #14406
                                                                                                                                          02-DEC-2004 (first entry)
Query Match
Best Local Similarity 63.0
Best Local 7; Conservative
                                                   |: |||| :||
255 AATAAARAIDY 265
                                          1 ASIAAARVLDY 11
                                                                                                                                                                                                                                                                                                                                           HINKLE G J.
SLATER S C.
CHEN X.
                                                                                                                                                                                                                                                                                                                                                                         (GOLD/) GOLDMAN B S.
                                                                                                                                                                                                                                                                  US2003233675-A1.
                                                                                                                                                                                                                                                                                   18-DEC-2003.
                                                                                                                         ADS25373;
                                                                                                                                                                                                                                                  Bacteria.
                                                                                                                                                                                                                                                                                                                                                                                         Cao Y,
                                                                                                                                                                                                                                                                                                                                                        (SLAT/)
(CHEN/)
                                                                                                                                                                                                                                                                                                                                       CAOY/)
                                                                                                                                                                                                                                                                                                                                                HINK/
                                                                                      RESULT 7
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a crop plant comprised property. The plant is a crop plant contrained property comprises transformed plant, where the polynucleotide or polypeptide is useful for improving plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant with the improved plant properties. Cr the recombinant DNA construct is useful for improving plants with improved plant properties, e.g. improved cold, heat or a drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or peets, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth rayled and/or content, improved yield by modified seed oil or protein yield and/or content, improved yield by modification of photosynthesis or by property or property or property or property. New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties. Claim 1; SEQ ID NO 14406; 122pp; English

one stress providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.

88888888888

Sequence 655 AA;

72.0%; Score 36; DB 8; Length 655; 63.6%; Pred. No. 1.6e+02; ive 2; Mismatches 2; Indels Local Similarity 63.6 1 ASIAAARVLDY 11 Query Match Best Loc Matches

|: |||| :|| 255 AATAAARAIDY 265 셤

ADS22602 standard; protein; 656 AA. 02-DEC-2004 (first entry) ADS22602; RESULT 8

ADS22602

ID ADS2602

XX ADS2

XX ADS2

XX ADS2

XX Recc

XW Recc

XW Recc

XW Recc

XW Recc

XW Bact

XX CA

XX CA

XX CA

XX CA

XX CC

Bacterial polypeptide #11635.

Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

Bacteria.

US2003233675-A1

18-DEC-2003

20-FEB-2003; 2003US-00369493

21-FEB-2002; 2002US-0360039P

CAO Y.
HINKLE G J.
SLATER S C.
CHEN X.
GOLDMAN B S. (CAOY/) (HINK/) )

(SLAT/) (CHEN/) (GOLD/)

Chen X, Goldman BS; Slater SC, Hinkle GJ, Cao Y,

WPI; 2004-061375/06.

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 11635; 122pp; English.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant baving an improved property comprises transforming a plant with the recombinant DNA construct and attensforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with

improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress production, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

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Gaps

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Sequence 656 AA,

Gaps ö Score 36; DB 8; Length 656; Pred. No. 1.7e+02; 2; Mismatches 2; Indels Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative ;

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|: |||| :|| 255 AATAAARAIDY 265 1 ASIAAARVLDY 11 셤 ઠે

ABB48560 standard; protein; 708 AA. ABB48560 ID ABB4

(first entry) 05-FEB-2002

Listeria monocytogenes protein #1264.

Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.

Listeria monocytogenes.

WO200177335-A2

18-OCT-2001.

11-APR-2001; 2001WO-FR001118.

11-APR-2000; 2000FR-00004629.

(INSP ) INST PASTEUR

Cossart P; Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Dussurget O, Chetouani P, Nedjari H, Glaser P, Kunst F, Cossart I Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L, Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Hadunio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J; Rose M, Voss H; 

WPI; 2002-010914/01.

Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related polypeptides.

Claim 6; SEQ ID NO 1265; 192pp; French.

of L The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments it are useful for selecting probes and primers for detecting genes in monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins

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expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially blosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fire.wipo.int/pub/published_pct_sequences
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99US-0126748P.
99US-0128734P.
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99US-0131449P.
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697 AAARIIDY 704
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05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
19-APR-1999;
19-APR-1999;
21-APR-1999;
21-APR-1999;
21-APR-1999;
06-MAY-1999;
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06-MAY-1999;
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PR 18-MAY-1999; 99US-0114768P.
PR 20-MAY-1999; 99US-01351234P.
PR 21-MAY-1999; 99US-01351234P.
PR 21-MAY-1999; 99US-01351234P.
PR 22-MAY-1999; 99US-0136324P.
PR 23-MAY-1999; 99US-0136324P.
PR 03-UN-1999; 99US-01377224P.
PR 03-UN-1999; 99US-01377224P.
PR 10-UN-1999; 99US-01377224P.
PR 11-UN-1999; 99US-0134658P.
PR 12-UN-1999; 99US-0134658P.
PR 13-UN-1999; 99US-0134658P.
PR 13-UN-1999; 99US-0134658P.
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PR 23-UN-1999; 99US-0134658P.
PR 23-UN-1999; 99US-0134658P.
PR 13-UN-1999; 99US-0140353P.
PR 13-UN-1999; 99US-0140353P.
PR 13-UN-1999; 99US-0143342P.
PR 13-UN-1999; 99US-0143342P.
PR 13-UN-1999; 99US-0143342P.
PR 13-UN-1999; 99US-0143332P.
PR 13-UN-1999; 99US-0143342P.
PR 13-UN-1999; 99US-0144334P.
PR 13-UN-1999; 99U
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PR 27-JUL-1999; 99US-0145919P.
PR 02-AUG-1999; 99US-014638EP.
PR 02-AUG-1999; 99US-014638EP.
PR 02-AUG-1999; 99US-014638EP.
PR 02-AUG-1999; 99US-01438EP.
PR 03-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-014732EP.
PR 05-AUG-1999; 99US-01473EP.
PR 11-AUG-1999; 99US-01431EP.
PR 12-AUG-1999; 99US-01431EP.
PR 12-AUG-1999; 99US-014912EP.
PR 13-AUG-1999; 99US-014912EP.
PR 20-AUG-1999; 99US-014913EP.
PR 21-AUG-1999; 99US-014913EP.
PR 21-AUG-1999; 99US-014913EP.
PR 22-AUG-1999; 99US-014913EP.
PR 23-AUG-1999; 99US-015105EP.
PR 24-SEP-1999; 99US-015105EP.
PR 25-SEP-1999; 99US-015105EP.
PR 25-SEP-1999; 99US-015105EP.
PR 25-SEP-1999; 99US-015105EP.
PR 26-SEP-1999; 99US-015105EP.
PR 13-CCT-1999; 99US-015105EP.
PR 13-CCT-1999; 99US-015105EP.
PR 13-CCT-1999; 99US-015903P.
PR 13-CCT-1999; 99US-01603P.
PR 27-CCT-1999; 99US-0160
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                                                                                Query Match 68.0%; Score 34; DB 3; Length 157; Best Local Similarity 100.0%; Pred. No. 90; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                             Zea mays protein fragment SEQ ID NO: 19947
                                                                                                                                                                                              AAG18509 standard, protein, 159 AA.
99US-0161359P.
99US-0161360P.
99US-0161361P.
99US-0161920P.
99US-0161932P.
99US-016193P.
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990S-012348P.
990S-012548P.
990S-0126264P.
990S-012624P.
990S-0128234P.
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26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
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29-0CT-1999;
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05-MAR-1999;

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16-APR-1999;

16-APR-1999;

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10-APR-1999;

11-MAY-1999;

12-MAY-1999;

12-MAY-1999;

13-MAY-1999;

13-MAY-1999;

14-MAY-1999;

15-MAY-1999;

16-MAY-1999;

17-MAY-1999;

18-MAY-1999;

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US-0147302P US-0147192P US-0147303P US-0147303P US-0147436P US-0147935P US-0148313P US-0148341P US-0148341P US-0148341P US-0148341P US-0149368P	US-01491759 US-01491729 US-014991729 US-01499029 US-0150666 US-01510669 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069 US-0151069	99US-0157117P. 99US-0157753P. 99US-0158023P. 99US-0158232P. 99US-0158232P. 99US-0159234P. 99US-0159234P. 99US-0159234P. 99US-0159234P. 99US-0159234P. 99US-0159234P. 99US-0159234P. 99US-015923P. 99US-015933P. 99US-015933P. 99US-0160767P. 99US-0160768P. 99US-0160768P. 99US-0160768P. 99US-0160768P. 99US-0160768P. 99US-0160768P. 99US-0160768P. 99US-0160768P. 99US-0160768P. 99US-016081P. 99US-016081P. 99US-016081P. 99US-016081P. 99US-016081P. 99US-016081P.
04-AUG-1999 05-AUG-1999 05-AUG-1999 06-AUG-1999 09-AUG-1999 11-AUG-1999 11-AUG-1999 13-AUG-1999 13-AUG-1999	15-AUG-1999 18-AUG-1999 20-AUG-1999 20-AUG-1999 20-AUG-1999 21-AUG-1999 21-AUG-1999 27-AUG-1999 27-AUG-1999 27-AUG-1999 27-AUG-1999 27-AUG-1999 27-AUG-1999 27-AUG-1999 27-AUG-1999 27-AUG-1999 27-AUG-1999 27-AUG-1999 27-AUG-1999 27-AUG-1999 27-AUG-1999 28-SEP-1999 28-SEP-1999 28-SEP-1999 28-SEP-1999	1515151515151515151515151515151515151515

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Vaccine, eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogramulomatosis.
                                  68.0%; Score 34; DB 3; Length 159; 100.0%; Pred. No. 91; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of a Chlamydia trachomatis protein.
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                                                                                                                                                                                                                                                                                                                                                                                                     AAY37904 standard; protein; 180 AA
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97FR-00016034.
98US-0107077P.
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Query Match
Best Local Similarity 100.00
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04-NOV-1998;
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AAXX

AAX.

AAX.

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AAY36754-Y37949 are encoded by open reading frames (ORFS) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogramulomatosis. The polypeptides of the invention may be of use in treating these diseases

Sequence 180 AA;

Gaps ö Length 180; 1; Indels Score 34; DB 2; Pred. No. 1e+02; 1; Mismatchee 68.0%; £ Best Local Similarity 77.8 Matches 7; Conservative Query Match

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11 3 IAAARVLDY

RESULT 13 ADS28058 ID ADS28058 standard; protein; 231 AA.

ADS28058;

02-DEC-2004 (first entry)

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Gaps

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Bacterial polypeptide #17091.

Recombinant DNA construct, transformed plant, improved plant property, cold tolerance; hear tolerance; drought tolerance; brebicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

US2003233675-A1. 

8-DEC-2003

20-FEB-2003; 2003US-00369493

21-FEB-2002; 2002US-0360039P.

CAO Y. HINKLE G J. SLATER S C. (CAOY/) (HINK/)

(SLAT/) SLATER S C. (CHEN/) CHEN X. (GOLD/) GOLDMAN B S.

Goldman BS; Chen X, Hinkle GJ, Slater SC, Cao Y,

WPI; 2004-061375/06.

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 17091; 122pp; English.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant with the ecombinant DNA construct and growing the transformed plant with the crecombinant DNA construct and growing the transformed plant with the polynucleotide or polypeptide is useful for improving plant properties.

The recombinant DNA construct is useful for improving plants with construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plants with construct is useful for improving plants with construct is useful for improving plants with construct is useful for producing plants with construct to plant disease, better growth rate by modification of content, improved plant disease, better growth rate by modification of the plant growth and development under at least one stress condition, improved light production or improved galactomannan condition, improved light production or improved galactomannan condition. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence cate for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.thml.

Sequence 231 AA;

Gaps ö 68.0%; Score 34; DB 8; Length 231; 80.0%; Pred. No. 1.4e+02; ive 1; Mismatches 1; Indels Query Match
Best Local Similarity 80.0
Matches 8; Conservative

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1 ASIAAARVLD 10

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990S-0139455P.
990S-0139456P.
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990S-0139461P.
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990S-0144333P.
990S-014584P.
18-JUN-1999;

22-JUN-1999;

23-JUN-1999;

22-JUN-1999;

23-JUN-1999;

23-JUL-1999;

24-JUN-1999;

25-JUL-1999;

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¹¹ AARVLDY AARVLDY S

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APPLICANT: van den Ouweland, Anna Maria Wilhelmina
APPLICANT: van den Ouweland, Anna Maria Lambertus Petrus
APPLICANT: Nobroek, Antonius Johannes Maria
APPLICANT: Koning, Piet Nico Maria
TITLE OF INVENTION: Endoproceolytic Activity; A Process for
TITLE OF INVENTION: Endoproceolytically Processing (Precursor);
TITLE OF INVENTION: Endoproceolytically Processing (Precursor);
TITLE OF INVENTION: Production of Proteins
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPPE
Endoproteolytic Activity; A Process for
Endoproteolytically Processing (Precursor)
Proteins And For The (Micro)Biological
Production Of Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 2; Length 278;
Pred. No. 25;
0; Mismatches 2; Indels
TITLE OF INVENTION: Endoproteolytical:
TITLE OF INVENTION: Endoproteolytical:
TITLE OF INVENTION: Proteins And For:
TITLE OF INVENTION: Proteins And For:
TITLE OF INVENTION: Proteins And For:
TITLE OF INVENTION: Protein Of Proteins And For:
CORRESONDENCES: 12
CORRESSEE: HOFFMANN & BARON, LLP
STREET: 350 Jericho Turnpike
CITY: Jericho
STREET: 350 Jericho Turnpike
CITY: Jericho
STREET: BAW YORK
COMPUTER: US.A.
ZIP: 11753
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BAP FORD:
COMPUTER: PARE FORM:
MEDIUM TYPE: POPPY disk
COMPUTER: PARE FORM:
MEDIUM TYPE: 29-MAY-1997
CLASSIFICATION NUMBER: US/08/865,203
FILLING DATE: 29-MAY-1997
CLASSIFICATION NUMBER: 40,846
REFERENCE/DOCKET UNBER: 294-41 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3582
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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amino acid
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-865-203-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 ASILAVRVLD 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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Pred. No. 30;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                       Score 46; DB 4; Length 11;
Pred. No. 0.0013;
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Patent No. 5935815
GENERAL INFORMATION:
APPLICANT: van de Ven, Willem Jan Maria Wilhelmina
APPLICANT: van de Ouweland, Anna Maria Wilhelmina
APPLICANT: van Duijnhoven, Johannes Lambertus Petrus
APPLICANT: Non Duijnhoven, Johannes Maria
APPLICANT: Robroek, Antonius Johannes Maria
APPLICANT: Koning, Piet Nico Maria
TITLE OF INVENTION: Pharmaceutical Composition Having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09342648

| Sequence 2, Application US/09342648
| Patent NO. 6248584
| GENERAL INFORMATION:
| APPLICANT: Cahoon, Rebecca E. APPLICANT: Cahoon, Rebecca E. APPLICANT: APPLICANT: APPLICANT: Mafalski, Antoni
| TITLE OF INVERTION Transcription Coactivators FILE REFERENCE BB-1169-B
| CURRENT FILING DATE: 1999-06-29
| CURRENT FILING DATE: 1999-06-29
| EARLIER APPLICATION NUMBER: 60/092,659
| EARLIER PILING DATE: July 13, 1998
| NUMBER OF SEQ ID NOS: 10
| SOFTWARE: Microsoft Office 97
| LENGTH: 755
                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                     CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 19
LENGTH: 11
                CURRENT APPLICATION NUMBER: US/09/383,667
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Best Local Similarity 90.9
Matches 10; Conservative
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1 ASIAAGRVLDY 11
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US-09-383-667-19
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Best Local Similarity
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ORGANISM: Zea mays
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LOCATION: (179)
FEATURE:
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LOCATION: (241)
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US-08-865-203-6
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LENGTH: 278 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-253-854-6
                      SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acio
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APPLICANT: van den Ouweland, Anna Maria Wilhelmina;
APPLICANT: van den Ouweland, Anna Maria Wilhelmina;
APPLICANT: van buijnhoven, Johannes Lambertus Petrus;
APPLICANT: Robroek, Antonius Johannes Maria; and
APPLICANT: Roning, Piet Nico Maria
ITILE OF INVENTION: Pharmaceutical Composition Having An
ITILE OF INVENTION: Endoproteolytically Processing (Precursor)
ITILE OF INVENTION: Proteins And For The (Micro) Biological
ITILE OF INVENTION: Production Of Proteins
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: 12
ADDRESSEE: HOFFMANN & BARON, LLP
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NAME: Tran, Jessica H.
REGISTRATION NUMBER: 40,846
REFERENCE/DOCKET NUMBER: 294-41 DIV II/CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/849,420
FILING DATE: 19920624
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MOCAN, Thomas F.
REGISTRATION NUMBER: 2805/41413
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQUENCE (212) 977-9550
TELERAX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
STRANDEDRESS: single
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STATE: New York
COUNTRY: U.S.A.
ZIP: 11753
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION NUMBER: US/09/253,854
FILING DATE: Unassigned
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-253-854-6; Sequence 6, Application US/09253854; Patent No. 6132717; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: HOFFMANN & BARON, 350 Jericho Turnpike
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Best Local Similarity 80.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-849-420-6
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96 ASILAVRVLD 105
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TELEX: INFORMATION FOR SEQ ID NO:

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1 ASIAAARVLD 10
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US-09-196-281-9
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5472855-6
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                                                                                                                          Score 34; DB 2; Length 279;
Pred. No. 25;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68.0%; Score 34; DB 4; Length 279;
80.0%; Pred. No. 25;
tive 0; Mismatches 2; Indels
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| Sequence 6. 658938
| GENERAL INFORMATION:
| APPLICANT: Hansen, Peter |
| APPLICANT: Hansen, Peter |
| APPLICANT: Mikkelsen, Frank |
| APPLICANT: Mikkelsen, Frank |
| APPLICANT: Andersen, Kim |
| TITLE OF INVENTION: Protease Variants and Compositions |
| TITLE OF INVENTION: Protease Variants and Compositions |
| CURRENT FILING DATE: 5348.204.US |
| CURRENT FILING DATE: 2000-02-29 |
| NUMBER OF SEQ ID NOS: 12 |
| SOFTWARE: Patentin version 3.1 |
| SEQ ID NO 6 |
| TENGRADE OF SEQ ID NOS: 12 |
| SEQ ID NO 6 |
| TENGRADE OF SEQ ID NOS: 12 |
| SEQ ID NOS: 13 |
| SEQ ID NOS: 13 |
| SEQ ID NOS: 14 |
| SEQ ID NOS: 15 |
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| SEQ ID NOS: 16 |
| SEQ ID NOS: 17 |
| SEQ ID NOS: 17 |
| SEQ ID NOS: 18 |
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Patent No. 655355

GENERAL INFORMATION:
APPLICANT: Hansen, Peter
APPLICANT: Bauditz, Peter
APPLICANT: Mikkelsen, Kim
APPLICANT: Andersen, Kim
FILE REFERENCE: 5349.204-US
CURRENT APPLICATION NUMBER: US/09/512,251A
CURRENT APPLICATION NUMBER: 1200-02-24

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1
                                                                                                                                        Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-135-658-4
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Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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96 ASILAVRVLD 105
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CORGANISM: Bacillus
US-09-515-150A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Bacillus
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80.0%; Pred. No. 25;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 4; Length 279;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
Sequence 9. Application US/09196281A; Sequence 9. Application US/09196281A; Patent No. 6605458; GENERAL INFORMATION: APPLICANT: Bansen, Peter K.; APPLICANT: Bandliz, Peter K.; APPLICANT: Mikkelsen, Frank; TILE OF INVENTION: Protease Variants And Compositions; FILE REFERENCE: 5435.200-US; CURRENT FILING DATE: 1999-11-19; CURRENT FILING DATE: 1997-11-21; NUMBER OF SEQ ID NOS: 18; SOFTWARE FESTSCE for Windows Version 3.0; SEQ ID NO 9; SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5472855

Patent No. 5472855

Patent No. 5472855

TITLE OF INVENTION: SUBSTRATE ASSISTED CATALYSIS

NUMBER OF SEQUENCES: 31

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/287,964

FILING DATE: 22-SEP-1994

PRIOR APPLICATION NUMBER: 90,902

FILING DATE: 12-JUL-1993

APPLICATION NUMBER: 923,039

FILING DATE: 14-JAN-1992

APPLICATION NUMBER: 35,652

FILING DATE: 06-APR-1987

APPLICATION NUMBER: 34,081

FILING DATE: 01-APR-1986

APPLICATION NUMBER: 846,627

FILING DATE: 01-APR-1986

APPLICATION NUMBER: 886,594

FILING DATE: 29-MAY-1984

APPLICATION NUMBER: 614,615

FILING DATE: 29-MAY-1984

APPLICATION NUMBER: 614,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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Score 33; DB 4; Length 85; Pred. No. 9.8; 1; Mismatches 2; Indels

Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative

; OTHER INFORMATION: Gap in alignment; FEATURE:
; NAME/KEY: MISC FEATURE
; LOALTION: (30)...(33)
; OTHER INFORMATION: Gap in alignment US-09-698-286A-10

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96 ASILAVRVLD 105

S00Z 0Z:65:01 c

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RESULT 13
SPATORSES
FATORSES
FATORSES
TITLE OF INVENTION'S GUBSTRAITE ASSISTED CATALYSIS
INTREL OF INVENTION'S GUBSTRAITE ASSISTED CATALYSIS
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
FILING DATE: 12-301-1993
APPLICATION NUMBER: 90,902
FILING DATE: 12-301-1993
APPLICATION NUMBER: 90,902
FILING DATE: 04-AR-1992
APPLICATION NUMBER: 35,622
FILING DATE: 04-AR-1989
APPLICATION NUMBER: 134,081
FILING DATE: 01-AR-1989
APPLICATION NUMBER: 134,081
FILING DATE: 01-AR-1989
APPLICATION NUMBER: 134,081
FILING DATE: 01-AR-1989
APPLICATION NUMBER: 614,612
FILING DATE: 20-AR-1984
APPLICATION NUMBER: 614,612
FILING DATE: 20-AR-1984
APPLICATION NUMBER: 614,615
FILING DATE: 20-MAY-1984
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Query Match
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Astarary Match
Db 96 ASILAVRVLD 105

RESULT 14
US-09-698-286A-10
: Sequence 10, Application US/09698286A
: Patent No. 6677442
: GENERAL INFORMATION: Human REVI Gene and Protein As Diagnostic, Preventive, and Therap FILE REPERBORD: 2000-10-30
: FILE REPERBORD: 2000-10-30
: FILE REPERBORD: 1999-10-29
: CURRENT APPLICATION NUMBER: 06/162,140
: PRIOR APPLICATION NUMBER: 60/162,140
: PRIOR APPLICATION NUMBER: 60/162,140
: PRIOR APPLICATION NUMBER: 60/162,140
: PRIOR PILING DATE: 1999-10-29
: NUMBER OF SEQ ID NOS: 39
: SEQ ID NOS: 39
: SEQ ID NO 10
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TYPE: FRT

OKGANISM: C. elegans, A. thaliana, S. cerevisiae, S. pombe and H. sapiens
FEATURE:
NAME/KEY: MISC FEATURE
OCCATION: (17) -. (22)
OTHER INFORMATION: Gap in alignment

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October 14, 2005, 16:20:10; search time 78.2031 Seconds (without alignments) 58.615 Million cell updates/sec
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2: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Perfect score:
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RESULT 1	US-10-425-115-369042	; Sequence 369042, Application US/10425115	; Publication No. US20040214272A1	; GENERAL INFORMATION:	; APPLICANT: La Rosa, Thomas J.	; APPLICANT: Kovalic, David K.	; APPLICANT: Zhou, Yihua	; APPLICANT: Cao, Yongwei	; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules associated with	; TITLE OF INVENTION: Plants	; FILE REFERENCE: 38-21 (53222) B	; CURRENT APPLICATION NUMBER: US/10/425.115	; CURRENT FILING DATE: 2003-04-28	; NUMBER OF SEQ ID NOS: 369326	; SEQ ID NO 369042	; LENGTH: 183	; TYPE: PRT	; ORGANISM: Zea mays	; FEATURE:	; NAME/KEY: unsure	; LOCATION: (1)(183)	; OTHER INFORMATION: ungure at all Xaa locations	; FEATURE:	; OTHER INFORMATION: Clone ID: MRT4577_99740C.1.pep	02-10-425-115-369042	

ALIGNMENTS

2 SIAAARVLDY 11 |||| ||||| 91 SIAADRVLDY 100

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Gaps

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Query Match 80.0%; Score 40; DB 16; Length 183; Best Local Similarity 90.0%; Pred. No. 7.9; Matches 9; Conservative 0; Mismatches 1; Indels

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TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-10-425-115-208239
RESULT 4
US-10-425-115-208229
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Sequence 45544, Application US/10425114

Sequence 45544, Application WS. US20040034888A1

Sequence 45544, Application WS. US2004003488BA1

SENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Steven E

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313) B

CURRENT FILING DAPE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 455544

LENGTH: 573
                                                              Sequence 831, Application US/10389566
; Sequence 831, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
    APPLICANT: Monsanto Technology, LLC
    APPLICANT: Monsanto Technology, LLC
    APPLICANT: Laurie, Cathy C
    TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
    TILE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
    TILE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
    TILE OF INVENTION: NUMBER: US, 10/389, 566
    CURRENT FILING DATE: 2002-03-15
    PRIOR FILING DATE: 2002-06-25
    PRIOR FILING DATE: 2002-06-26
    NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PATCHIN VENTION 3.2
; SEQ ID NO 831
    LENGTH: 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KET: misc feature; Indextion: (103)...(104); LOCATION: (103)...(104); OTHER INFORMATION: Xaa can be any naturally occurring amino acid US-10-389-566-831
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74.0%; Score 37; DB 15; Length 408;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 8; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.0%;
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Best Local Similarity 72.7
Matches 8; Conservative
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ANIADTRVLDY 68
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Zea mays
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Con Yihua
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: WHOSE: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 208239
LENGTH: 694
Sequence 208229, Application US/10425115

Sublication No. US20040214272A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Eabou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Charte C. Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: US/10/425,115
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-65
SEQ ID NO 208229
LENGTH: 573
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Pred. No. 1.38+02;
1; Mismatches 2; Indels
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Pred. No. 1e+02;
1; Mismatches 2; Indels
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US-10-425-115-208239
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US-10-425-115-208229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 208239, Application US/10425115 publication No. US20040214272A1 GENERAL INFORMATION:
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Matches 8; Conservative
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179 ANIADTRVLDY 189
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Matches 8; Conservative
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Sequence 14406, Application US/10369493
; Sequence 14406, Application US/10369493
; Publication No. US2003023367541
; GENERAL INPORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Glodman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(5208)
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR PELLON DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14406
; TENCTU. CE
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; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwal
; APPLICANT: Slater, Steven C.
; APPLICANT: Slater, Steven C.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
; TITLE OF INVENTION: USANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: USANTS WITH IMPROVED
; TITLE OF SPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR PELLING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 47374
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                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 15; Length 65
Pred. No. 1.9e+02;
2; Mismatches 2; Indele
                 FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH: 652
                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-15165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14406
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                                                                                                                                                                                                                                                                                                                                             Query Match 72.0°
Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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255 AATAAARAIDY 265
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255 AATAARAIDY 265
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US-10-369-493-14406
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Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
ITLE OF INVENTION: US 60/360,039
FILE REFERENCE: 38-10 (5202-02-28
FRIOR RILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14688
LENGTH: 652
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Buckharcv, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
ITILE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
ITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
FURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 120758
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US-10-369-493-15165

i Sequence 15165, Application US/10369493

j Publication No. US20030233675A1

i GENERAL INFORMATION:
    APPLICANT: Gao, Yongweir
    APPLICANT: Steven C.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Coldman, Barry S.
    APPLICANT: Cheny S.
    APPLICANT: TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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Pred. No. 2.3e+02;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_2384C.1.pep
US-10-437-963-120758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: |||| :||
255 AATAAARAIDY 265
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                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Oryza sativa
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Score 35; DB 16; Length 45;
Pred. No. 18;
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_96731C.1.pep
US-10-437-963-201347
                                                                                                                                         0; Mismatches
                                                                                             70.0%;
                                                                                             Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                  2 SIAAARVLD 10
                                                                                                                                                                                                              16 SIATARVLD 24
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NAME/KEY: unsure
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US-10-767-701-38892
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; Sequence 20147, Application US/10437963
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; Publication No. US200401
; APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Wat, Wat
APPLICANT: Wat, Wat
APPLICANT: Wat, Wat
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rlants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT FILING DAMES: 2003-65-14
NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 201347
                                                                                                                                                                                                                                                                                                                                            Sequence 189048, Application US/10437963
Sequence 189048, Application US/10437963
Publication No. USZ0040123343A1
Sequence 189048, Application US/20040123343A1
SENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 189948
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72.0%; Score 36; DB 16; Length 1064;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 8; Conservative 1; Mismatches 1; Indel9 (
                                                                                                                       Query Match 72.0%; Score 36; DB 15; Length 656; Best Local Similarity 63.6%; Pred. No. 1.9e+02; Matches 7; Conservative 2; Mismatches 2; Indels
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US-10-437-963-189048
                                  ; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-11635
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255 AATAAARAIDY 265
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116 ASLAALRVLD 125
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ORGANISM: Oryza Bativa
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ORGANISM: Oryza sativa
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US-10-437-963-189048
                  LENGTH: 656
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Sequence 175236, Application US/10437963
; Sequence 175236, Application US/10437963
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; Rebrack Information:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Boukharov, Andrey A.
    APPLICANT: Butharov, Andrey A.
    APPLICANT: Li, Ping
    APPLICANT: Li, Ping
    APPLICANT: Li, Ping
    TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Rice Nucleic Acid Molecules and Uses Thereof for Plant Improvement
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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Sequence 38892, Application US/10767701
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Exou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(55535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT PILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 38892
LENGTH: 198
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10.0%; Score 35; DB 16; Length 107;
Best Local Similarity 80.0%; Pred. No. 45;
Matches 8; Conservative 1; Mismatches 1; Indels
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FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-C77436_1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT4530_73100C.1.pep
US-10-437-963-175236
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OTHER INFORMATION: unsure at all Xaa locations
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Page 5
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us-10-614-959-12.rapb
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C007 07.66.04

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RESULT 15
US-10-369-493-17091

is Sequence 17091, Application US/10369493

is Publication No. US20030233675A1

is GENERAL INPORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Gldman, Barry S.

APPLICANT: Gldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Gldman, Barry S.

APPLICANT: Goldman, Goldman, Goldman, Goldman, Goldman, Goldman, Goldman, Goldman, Goldm
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                                                                                                                                    Query Match 68.0%; Score 34; DB 16; Length 198; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 7; Conservative 0; Mismatches 0; Indel8
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114 AARVLDY 120
VUS-10-767-701-38892
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0; Gaps

Query Match 68.0%; Score 34; DB 15; Length 231; Best Local Similarity 80.0%; Pred. No. 1.6e+02; Matches 8; Conservative 1; Mismatches 1; Indels

Search completed: October 14, 2005, 17:00:43 Job time : 79.2031 secs

1 ASIAAARVLD 10 |:||||| || 100 ATIAAARKLD 109

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

October 14, 2005, 16:02:59 ; Search time 15.2969 Seconds (without alignments) 69.190 Million cell updates/sec Run on:

US-10-614-959-12 50 1 ASIAAARVLDY 11

Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	3-methylcrotonyl-C	3-methylcrotonyl-C	hypothetical prote	probable membrane	teichoic acid bios	carboxymethylenebu	thermitase (EC 3.4	sfere	hypothetical prote				probable DNA polym	conserved hypothet	hypothetical prote				cobyrinic acid a,c	glycine dehydrogen	glutamyl-tRNA synt		hypothetical prote	Œ		_	hypothetical prote	a	
SUMMARIES	91	AF2984	A98299	S43071	S56849	AE1210	D87715	SUMYTV	140371	T38883	B71468	AF1059	AF2831	B97609	F89878	G69213	T45400	C70858	C84904	A75619	H70463	G82104	845053	T27970	T06165	E85437	G69502	D64640	C87712	AG2869
	. DB	7	~	~	~	~	7	~	~	N	~	N	7	~	~	~	~	~	N	~	~	~	~	~	~	N	~	N	~	0
	Length	663	709	143	692	969	231	279	579	649	926	162	202	202	220	264	358	367	397	441	482	509	614	1027	1232	305	342	363	365	409
d	Query	72.0	72.0	70.0	70.0	70.0	68.0	68.0	68.0	68.0	68.0	0.99	99	0.99	0.99	0.99	66.0	0.99	0.99	0.99	0.99	99	0.99	99	66.0	64.0	64.0	64.0	64.0	64.0
	Score	36	36	35	35	35	34	34	34	34	34	33	33	33	33	33	33	33	33		33	33		33	33	32	32	32	32	32
	Result No.	-	7	М	4	'n	9	7	80	6	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	53

n-carbamoyl-beta-a hypothetical prote	hypoumetical proce probable ABC trans protein TINI5.9 (i probable xanthina	hypothetical prote hypothetical prote hypothetical prote	hypothetical prote hypothetical prote probable bacteriof	glutathione transf electron transfer electron transfer conserved hypothet
A97646 T20819	110230 B70558 G96524 G95940	T49642 T16347 AG2388	C75376 S75615 B83036	AF3541 A81001 F82018 AC3018
999	4 4 6 6	0 0 0	000	0000
415 435	576 655 777	817 119 131	144 172 177	230 249 254 254
0.49	64.0	62.0 62.0	62.0 62.0 62.0	62.0 62.0 62.0 63.0
322	9 9 9 6	317	3333	4444
30 31	. w w w 1 w 4 w	36 37 38	39 41 41	4 4 4 4 G E 4 70

## ALIGNMENTS

Arzby decides Agrobacterium tumefaciens (Statistics Agrobacterium tumefaciens (Statistics Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Accession: AF2084 (Statistics) (St

A;Gene: mccA A;Map position: linear chromosome C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoyl

ö . 0 Query Match 72.0%; Score 36; DB 2; Length 663; Best Local Similarity 63.6%; Pred. No. 27; Matches 7; Conservative 2; Mismatches 2; Indels

|: |||| :|| 258 AATAAARAIDY 268 1 ASIAAARVLDY 11

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RESULT 2

Gispecies: Agrobacterium tumefaciens
Cispecies: Agrobacterium tumefaciens
Ridoodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefarence number: Agriss; Mulb:21608551; PMID:11743194
A; Reference number: Agriss; Mulb:21608551; PMID:11743194
A; Molecule type: DNA
A; Residues: 1-709 < KUR>
A; Residues: 1-709 < KUR>
A; Consersion: Agriss Cispecies: A; Consersion: Agrobacterium tumefaciens: Leferences: UNIPROT:Q8UA95; GB:AE007870; PIDN:AAK89915.1; PID:g15159866; GSPDB:GAA; Genetics: A; Consersion: Agrabacterium tumefaciens Agrabacterium tumefaciens

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Query Match 70.0
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 70.0
Best Local Similarity 70.0
Matches 7; Conservative
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245 SLAAAIILDY 254
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A;Accession: S47117
A;Molecule type: DNA
A;Residues: 135-692 <VAW>
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A Molecule type: DNA
A, Residues: 1-696 <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: 1mo1085
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A; Cross-traceroces: EMBL:234288; NID:g498992; PIDN:CAA84049.1; PID:g498993
A; Cross-references: EMBL:234288; NID:g498992; PIDN:CAA84049.1; PID:g498993
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
Styandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
Submitted to the EMBL Data Library, June 1994
A; Description: Sequence analysis of a 17.1 kb DNA fragment from chromosome X of Sacchard
A; Reference number: S47117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-692 <ROS>
A;Residues: 1-692 <ROS>
A;Residues: 1-692 <ROS>
A;Cross-references: UNIPROT:P40358; EMBL:Z49348; NID:g1008228; PID:g1008229; MIPS:YJL073
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
submitted to the Protein Sequence Database, September 1995
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A; Reaidues: 135-692 «POH»
A; Cross-references: EMBL: Z49348; MIPS: YJL073w
A; Cross-references: EMBL: Z49348; MIPS: YJL073w
R; Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
A; Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
A; Title: Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevisia
A; Reference number: S50798; MUID: 95282514; PMID: 7762302
A; Accession: S50798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Status: nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Molecule type: LNA
A,Residues: 1-143 <THO->
A,Residues: 1-143 <THO->
A,CTOSS-references: UNIPROF.069582; EMBL:X73675; NID:9469952; FIDN:CAA52028.1; FID:94699
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: S43071
R; Thompson, J.; Choudhury, S.; Kashanchi, F.; Doniger, J.; Berneman, Z.; Frenkel, N.; Rc
A; Thompson, J.; Choudhury, S.; Kashanchi, F.; Doniger, J.; Berneman, Z.; Frenkel, N.; Rc
A; Title: A transforming fragment within the direct repeat region of human herpesvirus ty
A; Reference number: S43067; MUID: 94181269; PMID: 8134119
A; Rccession: S43071
          A,Map position: linear chromosome
C,Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy
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N.Alternate names: hypothetical protein HRC558; hypothetical protein J1083
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: S56849; S56789; S47117; S57736
R;Rose, M.; Koetter, P.; Entian, K.D.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S56849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: human herpesvirus 6
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
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                                                                                                        Query Match 72.0%; Score 36; DB 2; Length 709; Best Local Similarity 63.6%; Pred. No. 29; Matches 7; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein 5 - human herpesvirus 6
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|ASLAAARVL 15
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: D8712; Peldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.!
R;Nietand, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Haft, D.H.; Kolone
N, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shaphro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE1210
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, U. J; Kunh, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
A;Authors: Kreft, J.; Kunh, M.; Rust, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
A;Authors: Schueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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A;Experimental source: strain EGD-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        teichoic acid biosynthesis protein B homolog lmo1085 [imported] - Listeria monocytogenes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 692,
                                                                                                                                 A,Reference number: S57731
A,Accession: S57756
A,Accession: S57756
A,Residues: 1-692 <SOR>
A,Cross-references: EMBL:X88851; NID:g895892; PID:g895898
A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics:
A;Cross-references: EMBL:Z34288; NID:g498992; PID:g498993
R;Sor, F.J.
submitted to the EMBL Data Library, June 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 10L
C;Keywords: transmembrane protein
F;S85-655/Domain: dnaJ amino-terminal homology <DNJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.0%; Score 35; DB 2;
70.0%; Pred. No. 45;
tive 2; Mismatches
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hypothetical protein SPAC443.03c - fission yeast (Schizosaccharomyces pombe)
Gispecies: Schizosaccharomyces pombe
Gispecies: Schizosaccharomyces pombe
Gispecies: O3-bec-1999 #sequence_revision O3-bec-1999 #text_change O9-Jul-2004
GiAccession: T3883
Riwiply, L:, Harrist, D:, Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
A;Reference number: Z21807
A;Recession: T3883
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-649 *MUR>
A;Residues: 1-649 *MUR>
A;Residues: UNIPROT:Q10211; EMBL:Z69380; PIDN:CAA93342.1; GSPDB:GN0066; SPDB:SP)
G;Genetics: gtrain 972h-; cosmid C4H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dividable insulinase family/proteinase III - Chlamydia trachomatis (serotype D, strain UW; C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Species: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: B71468
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A;Fitle: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trach
A;Reference number: A71570; MUID:99000809; PMID:9784136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reaiduea: 1-956 <ARN>
A;Cross-references: UNIPROT:O84812; CB:AE001353; GB:AE001273; NID:93329271; PIDN:AAC6840;
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
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6.Species: Salmonella enterica subsp. enterica serovar Typhi
A.Note: this species has also been called Salmonella typhi
6.Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
6.Accession: AF1059
R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connecton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A.Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Tile: Complete genome sequence of a multiple drug resistant Salmonella enterica serove A;Reference number: AB0502; MUID:21534947; PMID:11677608
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A,Map position: 1
C,Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC4H3.03c
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Pred. No. 68;
2; Mismatches 1; Indels
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C;Superfamily: insulin-degrading enzyme (IDE)
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Best Local Similarity 70.0%;
Matches 7; Conservative
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631 AAIAAAHILD 640
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916 IAAARSMDY 924
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A,Status: preliminary
A,Molecule type: DNA
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A;Molecule type: DNA
A;Residues: 1-231 <STO>
A;Cross-references: UNIPROT:Q9A213; GB:AE005673; NID:g13425534; PIDN:AAK25720.1; GSPDB:G
C;Genetics:
A;Gene: CC3758
C;Superfamily: carboxymethylenebutenolidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Thermoactinomyces vulgaris
C;Species: Thermoactinomyces vulgaris
C;Accession: A00973
C;Accession: A00973
R;Meloun, B.; Baudys, M.; Kostka, V.; Hausdorf, G.; Frommel, C.; Hohne, W.E.
R;Meloun, B.; Baudys, M.; Kostka, V.; Hausdorf, G.; Frommel, C.; Hohne, W.E.
A;Title: Complete primary structure of thermitase from Thermoactinomyces vulgaris and it
A;Reference number: A00973
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A;Molecule type: DNA
A;Residues: 1-579 <RES>
A;Cross-references: UNIPROT:P43423; EMBL:X79509; NID:9619638; PIDN:CAA56041.1; PID:96196
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R;Rina, M.; Markaki, M.; Bouriotis, V.
Gene 150, 71-73, 1994
A;Title: Sequence of the cloned bseCIM gene: M.BseCI reveals high homology to M.BanIII.
A;Reference number: 140371; MUID:95047552; PMID:7959066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 1-279 AREL>
A; Residues: 1-279 AREL>
A; Cross-references: UNIPROT: P04072
C; Comment: This protein is enzymatically similar to a proteinase from Streptomyces sp. C; Superfamily: subtilisin; subtilisin homology
C; Keywords: hydrolase; serine proteinase
F; 29-239/Domain: subtilisin homology <SBT>
F; 29-239/Active site: Asp, His, Ser #status predicted
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C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                          Gaps
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C;Superfamily: site-specific methyltransferase (adenine-specific) PaeR7I
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80.0%; Pred. No. 28;
vative 0; Mismatches 2; Indels
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Pred. No. 23;
1; Mismatches
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Best Local Similarity 80.0%;
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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AEVIAKRILDY 36
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Best Local Similarity
Matches 6; Conserv
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Search completed: October 14, 2005, 16:23:38 Job time : 17.2969 Becs
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54.5%;
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Best Local Similarity 60.0%;
Matches 6; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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94 ASIAAVKLINY 104
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131 NVASASVLDY 140
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                                         156 ASIAAARAL 164
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A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: B97609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Datesion: AF2831
C;Accession: AF2831
C; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
C; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable DNA polymerase III, epsilon chain [imported] - Agrobacterium tumefaciens (strai
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
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A;Experimental source: strain C58 (Dupont)
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R;Godher, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA polymerase III, epsilon subunit [imported] - Agrobacterium tumefaciens (strain C58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gter, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Accession: AF2831
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                      A;Molecule type: DNA
A;Residues: 1-162 <PAR>
A;Residues: 1-162 <PAR>
A;Crosel-references: GB:ALS13382; PIDN:CAD06923.1; PID:g16505571; GSPDB:GN00176
C;Genetics:
A;Gene: STY4801
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66.0%; Score 33; DB 2; Length 202;
Best Local Similarity 88.9%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                 DB 2; Length 162;
26;
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88.9%; Pred. No. 32;
vative 0; Mismatches
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Pred. No. 26;
1; Mismatches
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A;Map_positTon: circular chromosome
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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112 AVARILDY 119
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A Molecule type: DNA
A Residues: 1-202 < KUR>
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A;Molecule type: DNA
A;Residues: 1-202 <KUR>
Status: preliminary
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conserved hypothetical protein SA0939 [imported] - Staphylococcus aureus (strain N315)
Conserved hypothetical protein SA0939 [imported] - Staphylococcus aureus
Conserved hypothetical protein 10-May-2001 #text_change 09-Jul-2004
Conserved hypothetical protein 10-May-2001 #text_change 09-Jul-2004
Conserved 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
Conserved 10-May-2001 #sequence 10-May-2001 #tori, N.; Sawano, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch
Robert 10-May-2001
Antitle: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
Antitle: Mayolecule type: DMS
Antitle: Mayolecule type: DM
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hypothetical protein MTH852 - Methanobacterium thermoautotrophicum
C; Species: Methanobacterium thermoautotrophicum
C; Space: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C; Accession: G69213
R; Smith, D.R; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; E
R; Smith, D.B; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functs
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functs
A; Aritle: Complete genome sequence of Methanobacterium translation not shown
A; Mesidues: 1-264 - WITH-
A; Mesidues: Mesidues:
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A;Experimental source: strain Delta H
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Pred. No. 43;
4; Mismatches 1; Indels
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Pred. No. 35;
3; Mismatches
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October 14, 2005, 15:51:44; Search time 73.2188 Seconds (without alignments) 76.932 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                 - protein search, using sw model
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BLOSUM62 Gapop 10.0 , Gapext 0.5 US-10-614-959-12 50 1 ASIAAARVLDY 11 Title: Perfect 'score: Sequence: Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
-	37	74.0	:	-	O6HR20	100000000000000000000000000000000000000
7	37	74.0	694	۱۸	OBERS	Osofed choman
m	37	74.0		N	0852E4	Oserez Birewallet
4	37	74.0		~	0861181	Obmis oryth
2	36	72.0		· ~	062CXB	Office Burkhold
9	36	72.0		۱ ۸	O63M18	O63mlg burkhold
7	36	72.0		~	08UA95	OSua95 agrobant
80	36	72.0		~	07CSK5	Ologhia egyphant
6	36	72.0		~	O8H034	OSPO24 CASTO
10	36	72.0		~	O7MA36	C7ma36 wolfnor
11	36	72.0		~	069X93	STRUCTURE COMING

O6h820 oryza sativ	Osefs2 shewanella	-	oryza	Q62cx8 burkholderi	_		Q7csk5 agrobacteri		woline			_		P40358 saccharomyc		_	-	N	m	~		_			-	_			bacillus	oryza sat	
2 Q6H820		2 Q8S2E4												L YJH3 YEAST	2 Q8Y8 <u>3</u> 3	2 Q6MK31	2 Q7R034	. Q6NA42	2 Q9A213		_	_	_	: Q9LS05	: Q9FV51	Q8P7L4	QBPIY6	MTC1 BACST	O9ROK2	Q7F1D1	
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37	37	37	37	36	36	36	36	36	36	36	32	32	32	32	32	35	32	34	34	34	34	34	34	34	34	34	34	34	34	34	
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Gaps QBEFS2 PRELIMINARY, PRT; 694 AA.

QBEFS2,

QBEFS .. o Query Match
74.0%; Score 37; DB 2; Length 421;
Best Local Similarity 80.0%; Pred. No. 69;
Matches 8; Conservative 1; Mismatches 1; Indels ||:|||| || 288 ASLAARALD 297 1 ASIAAARVLD 10 RESULT 2
QBEFS2
ID QBEFS2
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DT 01-M
DT 01-M
DT 01-M
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GN Shew
OC Bact
OC Bact
OC Shew
CC a ઠે

(1) SEQUENCE FROM N.A. STRAIN=MR-1; MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;

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Transferase. - - SEQUENCE 421 AA; 44979 MW; 7A996BBFFC673920 CRC64;

8 % R R R S

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waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Zhong H., Iwana H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y., Yano M., Jiang J., Gojobori T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50929; ABC_TM1F; 2.
PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.0%;
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les 7; Conservative
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Matches
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         Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A., Clayton R.A., Meyer T., Tsapin A., Soct J., Beanan M.J., Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., Mhite O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M., Lee C., Mueller J., Khouri H.M., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Shewanella oneidensis."; Shewanella oneidensis."; Shewanella oneidensis."; Rebell Aborton Rechond. 20:1118-1123(2002).
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PubMed=12447438; DOI=10.1038/nature01184;

Sasaki T. Matsumoto T. Yanamoto K., Sakata K., Baba T., Katayose Y.,

Sasaki T., Matsumoto T., Yanamoto K., Sakata K., Hanamoti H.,

Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,

Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,

Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,

Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,

Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,

Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,

Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakaura M.,

Nagasaki H., Nakashima M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,

Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Name=P0022F10.15;
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Stroptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.0%; Score 37; DB 2; I
54.5%; Pred. No. 1.1e+02;
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GO; GO: 0005524; F:ATP binding; IEA.
GO; GO: 000874; F:Bjotin binding; IEA.
GO; GO: 000874; F:Bjotin binding; IEA.
GO; GO: 0008872; F:Bjotin binding; IEA.
GO; GO: 0008812; P:RGGABO; IEA.
InterPro; IPRO05481; Biotin_GS.
InterPro; IPRO05481; Biotin_GS.
InterPro; IPRO05481; CPase L.N.
InterPro; IPRO05481; CPase L.N.
InterPro; IPRO11053; Hybrid_motif.
InterPro; IPRO11053; Hybrid_motif.
Pfam; PF00289; CPase L.Chain; I.
Pfam; PF00289; CPSase L.Chain; I.
Pfam; PF00289; CPSase L.Chain; I.
PROSITE; PS00189; BIOTIN; I.
PROSITE; PS00189; BIOTIN; I.
PROSITE; PS00189; BIOTIN; I.
PROSITE; PS00189; BIOTIN; I.
PROSITE; PS00086; CPSASE 2; UNKNOWN I.
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SEQUENCE 694 AA; 75656 1
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Best Local Similarity 54...
6; Conservative
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TIGR; SO1894; -.
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005264; F:ATP binding; IEA.
GO; GO:00042626; F:ATPaea activity, coupled to transmembrane m. . .; IEA.
GO; GO:0000166; F:Intelectide binding; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IRR011527; ABC membrane l.
InterPro; IPR011527; ABC membrane l.
InterPro; IPR001140; ABC_IM_transpt.
                                                                                                                                                                                                                                                                                                              transmembrane m. . ; IEA
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Jabinski M., Ducos E., Martinoia E., Boutry M.;
"The ATP-binding cassette transporters: structure, function and gene
"The ATP-binding cassette transporters: structure,
Family comparision between rice and Arabidopsis.";
Plant Physiol. 0:0-0(0).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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rano m., ulang J., Golobori T.;

"The genome sequence and structure of rice chromosome l.";

"The genome sequence and structure of rice chromosome l.";

Nature 420:312-316 (2002).

- !- SIMILARITY: Belongs to the ABC transporter family.

E MBAB; AP001229; BAB89499.1; -.

R Gramene; Q852E4; -.

R GO; GO:0016521; C:integral to membrane; IEA.

GO; GO:0016524; F:ATP binding; IEA.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0006810; P:transport; IEA.

R GO; GO:0006810; P:transport; IEA.

R GO; GO:0006810; P:transport; IEA.

R InterPro; IPR011527; ABC membrane l.

R InterPro; IPR011527; ABC membrane l.

R InterPro; IPR001439; ABC Transporter.

R Pfam; PF000664; ABC membrane; 2.

R Pfam; PF000065; ABC transporter; 2.

R Pfam; PF000055; ABC transporter; 2.

R Pfam; PF000055; ABC transporter; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 2; Length 1203;
Pred. No. 1.9e+02;
2; Mismatches 1; Indels
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
-i- SHILLARITY: Belongs to the ABC transporter family.
EMBL; AJ535055; CAD59577.1; -.
HSSP; PO8716; IMTO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1203 AA; 131506 MW; B7838BDC1B5F19AA CRC64;
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01.MAR-2003 (TrEMBLrel. 23, Last sequence update)
01.OCT-2003 (TrEMBLrel. 25, Last annotation update)
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InterPro; IPR003439; ABC_transporter.
Pfam; PF00064; ABC_membrane; 2.
Pfam; PF00005; ABC_tran; 2.
SWART; SM00382; AAA; 2.
SWART; SM00382; AAA; 2.
PROSITE; PS50229; ABC_TRANSPORTER 1; 2.
PROSITE; PS50831; ABC_TRANSPORTER 2; 2.
ATP-binding.
SEQUENCE 1234 AA; 134571 MW; CSF9E9D75D28AC93 CRC64;
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Gaps ö 74.0%; Score 37; DB 2; Length 1234; 70.0%; Pred. No. 2e+02; tive 2; Mismatches 1; Indels Query Match

Local Similarity 70.0 1 ASIAAARVLD 10 **datches** 

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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Major facilitator superfamily protein.
ORFNames=BMAA0712; 402 AA PRT; PRELIMINARY;

Burkholderia mallei ATCC 23344. Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia. NCBI_TaxID=243160;

SEQUENCE FOR.

STRAIN=ATCC 23344;

Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.B.,

Reldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C.,

Bavidson T.D., Deboy R.T., Dimitrow G., Dodson R.J., Durkin A.S.,

Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,

Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,

Selengud J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,

Zhou L., Fraser C.M.;

"Structural flexibility in the Burkholderia mallei genome.";

Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).

EMBL; CP000011; AAU46877.1;

SEQUENCE 402 AA; 41596 MW; 6FCA16BE0F4B18EA CRC64; SEQUENCE FROM N.A. RESULT 5
062CX8
10 062CC
AC 062CC
AC 062CC
DT 25-O
DT 25-O
DT 25-O
DE Majo
GN NEWN
OS BUCK
OC BUCK
OC

Length 402; 72.0%; Score 36; DB 2; Length 402 70.0%; Pred. No. 1.1e+02; ative 3; Mismatches 0; Indele Query Match 72.0 Best Local Similarity 70.0 Matches 7; Conservative

1 ASIAAARVLD 10

|::||||:|| 106 ATVAAARLLD 115

RESULT 6

Putative transporter protein. ORFNames=BPSS0842;

Burkholderia pseudomallei K96243. Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia. 063M18 PRELIMINARY, PRT, 402 AA. 263M18, TEMBLrel. 28, Created) 25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) NCBI_TaxID=272560; SEQUENCE FROM N.A. STRAIN=K96243; 063M18 11D QQQ DT 222 DT 222 DT 222 DG GN DT 2222 DG GN DT 22222 DG GN DT 2222 DG GN DT 22222 DG GN DT 2222 DG GN DT 22222 DG GN DT 2222 DG GN DT 22

ö Pubmed=15377794;

Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
A Atkins T., Crosenan L.C., Pitt T., Churcher C., Mungall K.,
Bentley S.D., Sebaihla M., Thomson N.R., Bason N., Beacham I.R.,
A Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
A Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,
Flitwall T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
Angelvilai S., Stewns K., Tumapa S., Vesaratchavear M.,
Angelvilai S., Stewns K., Tumapa S., Vesaratchavear M.,
Anitchead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
T. "Genomic plasticity of the causative agent of melioidosis,
Rutholderia pseudomallei.",
Roc. Natl. Acad. Sci. U. S. 101:14240-14245(2004).
EMBL; BX571966; CAH38304.1; -. Gaps . 0 72.0%; Score 36; DB 2; Length 402; 70.0%; Pred. No. 1.1e+02; tive 3; Mismatches 0; Indels Query Match
Best Local Similarity 70.0* 1 ASIAAARVLD 10 ઠે

|::||||:|| 106 ATVAAARLLD 115

RESULT 7 **Q8UA95** 

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SEQUENCE FROM N.A.

STRAIN-Dupont;

MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;

MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;

Moduza V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,

A chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chen Y., Clendenning J., Deatherage G., Gillet W., Grant C.,

M. Kutyavin T., Levy R., Li M.-J., McClalland E., Palmieri A.,

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

Angeng S., Yoo H., Tao Y., Biddle P., Jung M., Kreepan W., Perry M.,

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

B. Nester E.W.,

Science 294:2317-2323(2001).

EMBL, AR009278; AAL44292.1; -.

R. PIR, AR2984; AF2984.

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HSSP; P24182; LBNC.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005374; F:blocin binding; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
Pfam; PF02785; Biotin_carb C; I.
Pfam; PF02785; Biotin_lipyl; I.
Pfam; PF00289; CPSase_L chain; I.
PROSITE; PS00188; BTOTIN; I.
PROSITE; PS00188; BTOTIN; I.
PROSITE; PS00867; CPSASE_I; UNKNOWN I.
Biotin; Complete protecome.
SEQUENCE 663 AA; 71187 MW; 2366201C5F 

71187 MW; 2366201C5F36D292 CRC64;

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STRAIN=DSMZ 1740;

KRDLINE=22892897; PubMed=14500908; DOI=10.1073/pnas.1932838100;

MEDLINE=22892897; PubMed=14500908; DOI=10.1073/pnas.1932838100;

MEDLINE=22892897; PubMed=14500908; DOI=10.1073/pnas.1932838100;

MAGARIMAR R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,

Mandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,

Meyer F., Lederer H., Schuster S.C.;

Meyer F., Lederer H., Meyer H., Lederer H., Meyer H., Meyer H., Meyer H., Meyer H., Meyer H., Mey
                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.

Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Currie J.,

Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Preston R.,

Collura K., McCombie D.W.R., de la Bastide M., Spiegel L., Preston R.,

Kirchoff K., Kuit K., Nascimento L., Zutavern T., Balija V., Bell M.,

Baker J., Santos L., Miller B., Katzenberger F., Muller S., King L.,

Yang C., O'Shaugnessy A., Palmer L., Dedhia N.;

Submitted (JAN 2003) to the EMBL/Genbank/DDBJ databases.

EMBL, ACI19796, AAO17354.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLAGELIAR FUNCTIONAL PROTEIN.
Name=PFLA, OrderedlocusNames=W50490;
Wolinella succingenes.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Hypothetical protein OJ1172F09.9.

Name=OJ1172F09.9;

Oryza sativa (japonica cultivar-group).

Oryza sativa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldese; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.0%; Score 36; DB 2; Length 778; 63.6%; Pred. No. 2e+02; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.0%; Score 36; DB 2; Length 723; 80.0%; Pred. No. 1.9e+02; Live 1; Mismatches 1; Indels
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SEQUENCE 778 AA; 89775 MW; 3E2F992CE949C27E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 723 AA; 78613 MW; 3FD842215E6ED1FD CRC64;
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Q1-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Matches 7; Conservative
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InterPro; IPR008938; ARM.
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322 ASLAAVRLADY 332
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les 8; Conservative
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616 ASLAAARVTD 625
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Q69X93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agrobacterium tumefaciens (Gtrain C58 / ATCC 33970).
Bacteria; Proceobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
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Pred. No. 1.8e+02;
2; Mismatches 2; Indels
                             Score 36; DB 2; Length 663;
pred. No. 1.7e+02;
2; Mismatches 2; Indels
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Last sequence update)
Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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GO, GO.0005524; F.ATP binding; IEA.
GO, GO.0005524; F.ATP binding; IEA.
GO, GO.0016874; F.SIGase activity; IEA.
GO, CO.0001822; P.Metebolism; IEA.
GO, CO.0001822; P.Metebolism; IEA.
INTERPRO; IPRO01882; Biotin Garb C.
INTERPRO; IPRO01882; Biotin BS.
INTERPRO; IPRO01882; Biotin Lipoyl.
INTERPRO; IPRO01893; Biotin Lipoyl.
INTERPRO; IPRO019481; CPASE IN.
INTERPRO; IPRO11053; Hybrid motif.
InterPro; IPRO11054; Rudmit hyb_motif.
Pfam; PF002185; Biotin Carb C; I.
Pfam; PF002189; Biotin Lipoyl; 1.
PROSITE; PS00188; BIOTIN, 1.
PROSITE; PS00188; INTENNOWN I.
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                                        72.0%;
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Best Local Similarity 63.6
Matches 7; Conservative
           Ouery Match
Best Local Similarity 63.0.
The Conservative
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304 AATAAARAIDY 314
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01-OCT-2003
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SEQUENCE
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Q8H034;
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Q7CSK5
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084034 ID AC Q8 DT 01 DT 01

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"A transforming fragment within the direct repeat region of human herpesvirus type 6 that transactivates {\rm HIV-1."}_i, Oncogene 9:1167-1175(1994).
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-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. DB (GO: GO: GO: Ser. Protein serior) to the Ser/Thr protein kinase family. BE EMBL, APRO3562; BAD32908.1; -...

GO: GO: GO: GO: Serior Ser
                                                                                                                                          Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=94181269; PubMed=8134119;
Thompson J., Choudhury S., Kashanchi F., Doniger J., Berneman Z.,
Frenkel N., Rosenthal L.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                            Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
clone:P0633E08.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.0%; Score 36; DB 2; Length 1072; 80.0%; Pred. No. 2.7e+02; live 1; Mismatches 1; Indels
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                                                25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28; Last annotation update)
Putative receptor-like protein kinase 2.
Name=P0633E08.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human herpesvirus 6.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Roseolovirus.
NCBI_TaxID=10368;
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                   1072 AA
                   PRT;
                 PRELIMINARY;
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SEQUENCE FROM N.A.

STRAIN=LSV54 / DSM 12343;

PubMed=15305914;

Rabus R., Zibat A., Erickey T., Rattei T., Fartmann B., Stark M., Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K., Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R., Trent H.-P.;

The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium from permanently cold Arctic sediments.";

Environ. Microbiol. 6:887-902(2004).

Embl., CR522870; CAG35482.1;

Complete proteome.

SEQUENCE 184 AA; 20792 MW; 8D9DCBSEDFAA60AF CRC64;
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               Q6AQ91 PRELIMINARY; PRT; 184 AA.
Q6AQ91,
Q6AQ91,
25-OCT--2004 (TrEMBLrel. 28, Last sequence update)
25-OCT--2004 (TrEMBLrel. 28, Last sequence update)
25-OCT--2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
GrderediocusNames=DP0753,
DesulfocusNames=DP0753,
Bacteria, Proteobacteria, Deltaproteobacteria, Desulfoblaceae, Desulfotalea.
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NCBI_TaxID=1902;
                                                                                                                                                                                             Query Match 70.0%; Score 35; DB 2; Length 143; Best Local Similarity 88.9%; Pred. No. 63; Matches 8; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.0%; Score 35; DB 2; Length 184; 80.0%; Pred. No. 81; tive 2; Mismatches 0; Indels
[2] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. Thompson J.T., Thompson J.T., Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases. EMBL; X73675; CAA22028.1; -. FIR; 843071; S43071. SROUENCE 143 AA; 13317 MW; EDF78898C3D31734 CRC64; SROUENCE 143 AA; 13317 MW; EDF78898C3D31734 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9RJR7;
01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative zinc-binding oxidoreductase.
ORFNames=SCF51.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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| AAIAAARVLN 108
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STRAIN=A3(2) / M145;
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098JR7
AC 098JR
AC 098JR
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95282514; PubWed=7762302; Varietelle D., Hilger F.; Vandenbol M., Durand P., Dion C., Portetelle D., Hilger F.; Vandenbol M., Durand P., Dion C., Portetelle D., Hilger F.; Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces "Sequence includes the mitochondrial ribosomal protein LB."; Yeast 11:57-60(1995).
                                                                                                                                                                                                                                                    GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA. GO:0008270; F:zinc ion binding; IEA. InterPro; IPR012085; Adh zn family. InterPro; IPR011032; GroES_like. Pfam; PF00107; AH_zinc_N; I.
              Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
Rabbinowitesh B., Rajandream M.A., Rutherford K.M., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S.,
Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                 Hopwood D.A.;
"Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)";
Nature 417:141-147(2002).
EMBL; AL939105; CAB59716.1;
HSSP; Q8L3C8; 11XZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 44, Last annotation update)
Hypothetical 80.4 kDa protein in SMC3-MRRD4 intergenic region.
OrderedLocusNames=YJLO73W; ORFNames=J1083, HRC558;
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycetas; Saccharomycetas; Saccharomycetales; Saccharomycetas.
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to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
   MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
                                                                                                                                                                                                                                                                                                                                                             329 AA; 34155 MW; 5DCAD4FB174FD042 CRC64;
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189 SLGAAHVLDY 198
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Submitted (SEP-1995)
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                                                                                                                                                                                                                                                                                                                                               Complete proteome.
SEQUENCE 329 AA,
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ID YJH3_YEAST
AC P40358;
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                                                                                                                              GO; GG:0005783; C:endoplasmic reticulum; IDA.
GO; GG:000300; C:peripheral to membrane of membrane fraction; IDA.
GO; GO:0003767; F:co-chaperone activity; IGI.
GO; GO:000742; P:karyogamy during conjugation with cellular . . .; IGI.
GO; GO:000647; P:protein folding; IGI.
InterPro; IPR01623; DnaJ.N.
Pfam; PF00286; DnaJ. 1.
PROSITE; PS00636; DNAJ. 1; FALSE_NEG.
PROSITE; PS00636; DNAJ. 2; 1.
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692 AA; 80381 MW; 9F612DD16B66981B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                          Poly-Gln.
EMBL; X88851; CAA61312.1; -
EMBL; Z34288; CAA84049.1; -
PIR; S56849; S56849.
HSSP; BG022; BG2.
GermOnline; 141687; -.
SGD; S000003609; JEM1.
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245 SLAAAIILDY 254
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                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
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C007 17:60 of c

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mode1 - protein search, using sw OM protein

October 14, 2005, 15:51:19; Search time 99.9375 Seconds (without alignments) 50.310 Million cell updates/sec Run on:

US-10-614-959-13 66

Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 SGSTSNIGNNYVS 13 Sequence:

Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

A Geneseq 16Dec04:*

1: geneseqp1980s:*

2: geneseqp200s:*

4: geneseqp200s:*

5: geneseqp2001s:*

6: geneseqp2003s:*

7: geneseqp2003bs:*

8: geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	3071 Aav79071 Anti-fact	Aail02544 Anti	Autocoped	A21102612	DAILOSCALA	Aau02629 Ant	Aau02542	1 Aau02551 Ant	Abn45887 Hums	Adopt 4 singl	Ado34301 Neuroki	7 Ada34317	Abp45916	7 Aa031147 Himan	3 Adage743 Single	Ada34310 Neither	Adg34306	Ado34303	Abp45915	Ada96742 Sinal	Add98057 TNF OTO	Ade83862 Them	Ada34308	Ada34313	
)	DB ID	3 AAY7907	4 AAU02544	4 AAU02558			4 AAU02629	4 AAU02542	4 AAU0255:		7 ADG9671				6 AAO3114		8 ADG34310	8 ADG34306	8 ADG34303	5 ABP45915	7 ADG96742	7 ADG98057	8 ADE83862	8 ADG34308	8 ADG34313	
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Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		
·	score	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	
Result	S.	1	8	m	4	S	Q	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	•

Abp45906 Human BLy Ad996733 Single ch Ad996733 Single ch Ad6981372 Chemokine Abp45432 Human BLy Abp45432 Human BLy Abp45921 Human BLy Abp45962 Human BLy Abp45868 Human BLy Abp45868 Human BLy Ad930413 Human GMB Ad930455 Human GMB Ad930455 Single ch Ad996748 Single ch Ad996745 Single ch Ad996755 Single ch Ad996755 Single ch Ad996755 Single ch Ad996755 Single ch Ad996756 Single ch Ad996757 Single ch	1304
ABP45906 ADG96733 ADG96729 ABC83872 ABP45432 ABP45923 ABP45923 ABP45917 ABP45917 ABC30413 ADG30413 ADG96715 ADG96730 ADG96730 ADG96730 ADG96730 ADG96730	ADG34304
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22 24 44 44 44 44 44 44 44 44 44 44 44 4	247
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	99
2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	45

## ALIGNMENTS

RESULT 1 AAY7907.

AAY79071 standard; peptide; 13 AA.

AAY79071;

(first entry) 12-JUN-2000

Anti-factor IX/IXa antibody L chain V domain CDR1 amino acid sequence.

Complementarity determining region 1, CDR1; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; light chain; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metasteasis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC.

Homo sapiens.

WO200012562-A1.

09-MAR-2000.

99WO-US019453. 26-AUG-1999;

98US-0098233P. 99US-0122767P. 28-AUG-1998; 03-MAR-1999;

(GETH ) GENENTECH INC.

ä Kirchhofer Judice JK, Hass PE, Devaux B, Eaton DL, Adams CW, Suggett S;

WPI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

Claim 8; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 1 (CDR1) of the light chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXa is a vitamin K dependent plasma serime protease that participates in the blood coaqulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial 

Gapa

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100.0%; Score 66; DB 4; Length 109; 100.0%; Pred. No. 0.0026; ive 0; Mismatches 0; Indels

1 SGSTSNIGNNYVS 13

13, Conservative

Matches

Query Match Best Local Similarity

Sequence 109 AA;

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for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease

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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the far mass of an obese patient or the artibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a by complement mediated lysis. The antibodies may be labeled with a cells of etectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
               the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary angioplasty (PTCA), stroke, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular cosgulopathy (DIC)
and platelets. Compositions comprising the antibodies are used for
                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                         Length 13;
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                                                                                                                                                                                                                                                                         ; Score 66; DB 3; L; Pred. No. 0.00029; 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU02544 standard; protein; 109 AA.
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                                                                                                                                                                                                                                                                             100.0%;
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Best Local Similarity 100.
Matches 13; Conservative
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can be used as a therapeutic itself. Antibodise binding specifically to observe the used diseases. The antibodies can be used in the treatment of observy and observed diseases. The antibodies can be used in the treatment of observy and observed diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the far mass of an obses patient or the antibody can be used to activate the immune system to destroy the cells adjpocytes can be used to activate the immune system to destroy the cells of adjpocytes can be used to activate the immune system to destroy the cells of adjpocytes of an artibodies may be labeled with a consequence of adjpocyte antigen on the surface of an adjpocyte to detect or determine the presence or level of adjpocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for observations other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
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                                                                                                                                                                                                                                             Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
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llarity 100.0%; Pred. No. 0.0026;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                           Anti-adipocyte monoclonal antibody light chain, FAT 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 128-129; 182pp; English
                                                                                                      AAU02558 standard; protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaughan TJ;
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23 SGSTSNIGNNYVS 35
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ses 13; Conserva
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Best Local Si
Matches 13;
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                                                                                   AAU02558
ID AAU0
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AAU02627 standard; protein; 110 AA

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ઠે a AAU02612 standard; protein; 110 AA AAU02612;

(first entry) 29-AUG-2001

Anti-adipocyte monoclonal antibody light chain, FAT 99.

Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.

Homo sapiens

WO200127279-A1

19-APR-2001

11-OCT-2000; 2000WO-GB003900;

99US-0158812P 12-OCT-1999; (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Edwards BM, Main SH, Vaughan TJ,

WPI; 2001-282031/29. N-PSDB; AAS03512.

Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases.

Claim 1; Page 163; 182pp; English.

AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
cobssity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
cused in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intraabdominal fat associated with heart disease 

Sequence 110 AA;

Gaps ö 100.0%; Score 66; DB 4; Length 110; 100.0%; Pred. No. 0.0026; vative 0; Mismatches 0; Indels Conservative Query Match Best Local Similarity

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1 SGSTSNIGNNYVS 13 SGSTSNIGNNYVS 35

RESULT 5 AAU02627

AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain, complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
cobssity related diseases. The antibodies can be used to deliver drugs or
con be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
catectable label such as radiolabel, fluorescent or chemical group and
used in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
caterine other than undergoing surgery to remove excess farment. Antibodies
for different types of fat deposits can also be produced e.g. intraabdominal fat associated with heart disease Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related ö fat; Anti-adipocyte monoclonal antibody light chain, FAT 112. Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY. AAU02629 standard; protein; 110 AA. Claim 1; Page 172; 182pp; English. 11-OCT-2000; 2000WO-GB003900. 12-OCT-1999; 99US-0158812P (first entry) 23 SGSTSNIGNNYVS 35 1 SGSTSNIGNNYVS 13 Main SH, WPI; 2001-282031/29. Local Similarity N-PSDB, AAS03527 Sequence 110 AA; WO200127279-A1. Homo sapiens. 29-AUG-2001 Edwards BM, 19-APR-2001 diseases. Query Match Best Loca Matches RESULT 6
AAU02629
ID AAU0
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DT 29-P
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Gapa (first entry) 29-AUG-2001 AAU02629;

Anti-adipocyte monoclonal antibody light chain, FAT 113.

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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
cobesity related diseases. The antibodies can be used to deliver drugs or
cobesity related diseases. The antibodies can be used to deliver drugs or
con be used as a therapeuto: itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
con promplement mediated lysis. The antibodies may be labeled with a
complement mediated lysis. The antibodies may be labeled with a
complement mediated lysis. The antibodies may be labeled with a
consecutable label such as radiolabel, fluorescent or chemical group and
cused in methods of diagnosis in human subjects e.g. to determine the
constitution of the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
Contemnibodies can be used as an alternative means of treatment for obese
contemnibodies can be used as an alternative means of treatment for obese
content than undergoing surgery to remove excess fat. Antibodies
content types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
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                                                                                                                        CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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Matches 13, Conservative
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sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
obesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a thoraspeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
cycomplement mediated lysis. The antibodies may be labeled with a
detectable label such as radiolabel, fluorescent or chemical group and
used in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
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Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
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100.0%; Pred. No. 0.0026;
Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  Vaughan TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 173; 182pp; English
                                                                                                                                                                                                                                            11-OCT-2000; 2000WO-GB003900.
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N-PSDB; AAS03529.
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Best Local Similarity
Matches 13; Conserv
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                                                                                        Homo sapiens.
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(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Vaughan TJ;

Main SH,

Edwards BM,

WO200127279-A1

19-APR-2001

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Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related WPI; 2001-282031/29. N-PSDB; AAS03451. diseases 

ANU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
besity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the far mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies binding specifically to
by complement mediated lysis. The antibodies binding specifically
cation of adipocytes and the surface of an adipocyte to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intraabdominal fat associated with heart disease Claim 1; Page 124; 182pp; English.

Sequence 111 AA;

Gaps .; 0 100.0%; Score 66; DB 4; Length 111; 100.0%; Pred. No. 0.0027; Live 0; Mismatches 0; Indels Best Local Similarity 100. Matches 13; Conservative Query Match

1 SGSTSNIGNNYVS 13

ABP45887;

Human BLyS binding scFv SEQ ID 1898.

BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiALDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

15-JUN-2001; 2001WO-US019110.

16-JUN-2000; 2000US-0212210P. 17-OCT-2000; 2000US-0240B16P. 16-MAR-2001; 2001US-027624BP. 21-MAR-2001; 2001US-027379P. 25-MAY-2001; 2001US-0293499P.

ABP45887 standard; protein; 240 AA. 24 SGSTSNIGNNYVS 36 19-AUG-2002 (first entry) RESULT 9 g ઠે

Homo sapiens ABP45887

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WO200202641-A1. 10-JAN-2002 HUMAN GENOME SCI INC. CAMBRIDGE ANTIBODY TECHNOLOGY. (HUMA-)

Hilbert D; Vaughan T, Choi GH, Barash SC, WPI; 2002-114799/15. Ruben SM,

Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.

Claim 1; Page 2666-2667; 3148pp; English.

This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antithemmatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and immunodeficiency (e.g. common variable immunodeficiency (VID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of

Sequence 240 AA;

Gape ö Length 240; 100.0%; Score 66; DB 5; Length 24 100.0%; Pred. No. 0.0059; ive 0; Mismatches 0; Indele Query Match
Best Local Similarity 100.
Matches 13; Conservative

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ADG96714 standard; protein; 240 AA.

ADG96714;

(first entry) 11-MAR-2004

Single chain antibody that immunospecifically binds BLyS SeqID 1898

antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.

Unidentified

402003055979-A2.

10-JUL-2003.

14-NOV-2002; 2002WO-US036496.

16-NOV-2001; 2001US-0331469P. 19-DEC-2001; 2001US-0340817P. 

(HUMA-) HUMAN GENOME SCI INC

Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

WPI; 2003-505530/47.

Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g.

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New antibody that specifically binds neurokinin B, useful for preparing a composition for treating or preventing hypertension or preeclampsia.
rheumatoid arthritis, asthma and leukemia.
              Example 1; SEQ ID NO 1898; 394pp; English
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                                                                                                                                                                                                                                                                                                                                                 Neurokinin B antibody SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                     ADG34301 standard; protein; 242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2002; 2002US-0383802P.
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA, Ruben SM;
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N-PSDB; ADG34282.
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                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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The invention relates to a novel antibody specifically binding neurokinin B. An antibody of the invention has hypotensive, and gynaecological activity, and may have a use in gene therapy. The antibody is useful for preparing a composition for treating or preventing hypertension or preclampsia. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody; neurokinin B; hypotensive; gynaecological; gene therapy; hypertension; pre-eclampsia; NKB.
                                                                                                                                                                                                              100.0%; Score 66; DB 8; Length 242;
100.0%; Pred. No. 0.006;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2002; 2002US-0383802P
                                                                                                                                                                                                                                                                                                                                               154 SGSTSNIGNNYVS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                             1 SGSTSNIGNNYVS 13
                                                                                                                                                                                                                                                                  13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-053456/05.
                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADG34298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 242 AA;
                                                                                                                                                                          Sequence 242 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              402003102136-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                 invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG34317;
                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADG3431
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                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                               This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to thromosome 13434 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFve) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide. Or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods or present invention refers to the use of such antibodies in various methods corporated to the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders cuch, these compositions are useful for identifying immune disorders including myserbhania gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatorid arthritis, infectious diseases such as AIDS and proliferative disorders including leukamia, carcinoma and crivities such as antitheumatic, antiallergic and cytostatic. This activities such as antitheumatic, antiallergic and cytostatic. This cinvention. NOTE: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format of directely from WIPO at ftp.wipo.int/published pot_esquences.
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hypertension; pre-eclampsia; NKB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 66; DB 7; Length 240; 100.0%; Pred. No. 0.0059;
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                                                                                                                                      The invention relates to a novel antibody specifically binding neurokinin B. An antibody of the invention has hypotensive, and gynaecological estivity, and may have a use in gene therapp. The antibody is useful for preparing a composition for treating or preventing hypotrension or preciampsia. The present sequence is used in the exemplification of the
New antibody that specifically binds neurokinin B, useful for preparing composition for treating or preventing hypertension or preeclampsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 66; DB 8; Length 242; 100.0%; Pred. No. 0.006; ive 0; Mismatches 0; Indels
                                                                                           Claim 2; SEQ ID NO 40; 127pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 SGSTSNIGNNYVS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SGSTSNIGNNYVS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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RESULT 13 ABP45916

ABP45916 standard; protein; 243 AA. ABP45916; 

Human BLyS binding scFv SEQ ID 1927 (first entry) 19-AUG-2002

BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiALDS; vaccine; cancer; immune; auttoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

Homo sapiens

WO200202641-A1

10-JAN-2002.

15-JUN-2001; 2001WO-US019110

16-JUN-2000; 2000US-0212210P. 17-OCT-2000; 2000US-0240B16P. 16-MAR-2001; 2001US-027624BP. 21-MAR-2001; 2001US-0293499P. 25-MAY-2001; 2001US-0293499P.

(HUMA-) HUMAN GENOME SCI INC. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Hilbert Choi GH, Vaughan T, Ruben SM, Barash SC,

WPI; 2002-114799/15.

Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.

Claim 1; Page 2700-2701; 3148pp; English.

This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the E tumour necrosis factor (TMF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cycostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (e.g. common uired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent antibodies and fragments of the antibodies described in the method of acquired

Sequence 243 AA;

Gaps ô Local Similarity 100. Query Match Best Loca Matches

RESULT 14 AAO31147 ID AAO3

AAO31147 standard; protein; 243 AA

Human; protein coordinate data; heavy chain variable domain; VH; cancer; complementarity determining region; CDR; light chain variable domain; VL; TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5; DR5; TRAIL receptor 2; TRAIL R2; TNF-related apoptosis-inducing ligand; Kaposi, s sarcoma; central nervous system; medulloblastoma; neuroblastoma; glioblastoma; graft versus host disease; antibody therapy; nootropic; AIDS; acquired immune deficiency syndrome; neurodegenerative disorder; immunosuppressive; neuroprotective; antibody therapy; antibody. Human CM085C11 scFv protein that specifically binds TR7 ; 2002US-0369877P; ; 2002US-0384828P; ; 2002US-0396591P; ; 2002US-0403370P. 19-DEC-2002; 2002WO-US040597. 18-JUL-2002; 2002US-0396591P. 15-AUG-2002; 2002US-0403370P. 13-NOV-2002; 2002US-0425737P. 06-OCT-2003 (first entry) WO2003054216-A2. Homo sapiens 05-APR-2002; 04-JUN-2002; 03-JUL-2003 

Salcedo T, Albert VR, Rosen CA, Humphreys R, Vaughan TJ;

(HUMA-) HUMAN GENOME SCI INC.

WPI; 2003-569250/53. N-PSDB; AAL62844.

lung New antibody or its fragment, useful for treating, preventing or ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lurgastrointestinal cancer, or Kaposi's sarcoma or, graft versus host disease, AIDS

Claim 2; Page 288; 301pp; English.

The invention relates to an isolated antibody or its fragments such as WHCDR1 (heavy chain variable domain complementarity determining region), WHCDR2 (wHCDR2, VLCDR1 (light chain variable domain complementarity determining region), VLCDR2 or VLCDR3. The antibody or its fragment immunospecifically binds TRAIL (tumour necrosis factor; TNF-related appproals inducing ligand) receptor 7 (TRY). TRY is also referred to as TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and KILLER. The antibody or its fragment is useful for treating, preventing or ancieting an ancieting or ameliorating acancer. e.g. colon, breast, uterine, pancreatic, lung or gastrointestinal cancer or Kaposi's sarcome or cancer of the central nervous system such as medulloblastoma in neuroblastoma or glioblastoma or graft versus host disease, AIDS (acquired immune deficiency syndrome) or neurodegenerative disorder. The invention is useful in antibody nerapy. The present sequence is human scFv protein that specifically

Sequence 243 AA;

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Gape ö 100.0%; Score 66; DB 6; Length 243; 100.0%; Pred. No. 0.006; 1.1ve 0; Mismatches 0; Indels Local Similarity 100. Query Match

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1 SGSTSNIGNNYVS 13

155 SGSTSNIGNNYVS 167

Db

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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 13d4 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvB) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polyapptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The fragment invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the abstrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple solerosis, inflammatory disorders huma and rheumatorid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antihematic, antiathritic, neuroprotective, antiathrimatic, antiathritic, neuroprotective, antihitial mammatory, antiasthmatic, antiathritic, neuroprotective, antiathritic sequence is a single chain antibody that binds BLyS of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in the performat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
                                                                                                                                            Single chain antibody that immunospecifically binds BLyS SeqID 1927.
                                                                                                                                                                                      antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myashtenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; cardinoma; lymphoma; antirheumatic; antiathritic; neuroprotective; entiinflammatory; antiasthmatic; antiallergic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        directely from WIPO at ftp.wipo.int/pub/published pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaughan TJ, Hilbert D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 1927; 394pp; English
                ADG96743 standard; protein; 243 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chot GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-NOV-2002; 2002WO-US036496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-NOV-2001; 2001US-0331469P.
19-DEC-2001; 2001US-0340817P.
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                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                      11-MAR-2004
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                                                               ADG96743;
ADG96743
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Query Match 100.0%; Score 66; DB 7; Length 243; Best Local Similarity 100.0%; Pred. No. 0.006; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps

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Search completed: October 14, 2005, 16:12:41

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Job time : 100.938 secs

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RESULT 2
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-665-202-37
US-08-665-202-42
US-08-665-202-43
US-08-665-202-43
US-08-983-607-35
US-09-315-574-42
US-09-315-574-42
US-09-315-574-43
US-09-315-574-43
US-09-315-574-43
US-09-315-574-19
US-09-490-070A-18
US-09-490-070A-18
US-09-490-153-18
US-09-400-153-18
                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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US-09-956-087-4
US-09-420-592A-7
US-09-985-442-7
US-09-983-580-7
                                                                                                                                                                                                                                                                                                         513545 seqs, 74649064 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      protein search, using sw model
                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                            US-10-614-959-13
66
1 SGSTSNIGNNYVS 13
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                          Searched:
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No.
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 Sequence 15, Appl
Sequence 40, Appl
Sequence 112, Appl
Sequence 55, Appl
Sequence 32, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 51, Appl
Sequence 32, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 38, Appl
Sequence 38, Appl
Sequence 38, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 37, Application US/08665202;
Sequence 37, Application US/08665202;
Pattent No. 5977322;
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert;
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCES. 141
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
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                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/09383667

Patent No. 6624295

GENERAL INPORMATION:
APPLICANT: Adems, Camella W.
APPLICANT: Bacon, Dan L.
APPLICANT: Bacon, Dan L.
APPLICANT: Bacon, Dan L.
APPLICANT: Bacon, Dan L.
APPLICANT: Hass, Philip E.
APPLICANT: Widner, Daniel
APPLICANT: Sugger, Philip E.
APPLICANT: Sugger, Shelley
TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
CURRENT APPLICATION NUMBER: US/09/383,667
CURRENT APPLICATION NUMBER: US 60/098,233
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER PILING DATE: 1999-03-03
NUMBER OF EQ ID NOS: 32
SEQ ID NO 13
LENGTH: 13
           US-08-665-202-40
US-09-315-574-40
US-09-311-574-40
US-09-211-202-112
US-09-225-769B-32
US-09-025-769B-51
US-09-490-070A-32
US-09-490-153-32
US-09-490-153-32
US-09-490-153-51
US-09-490-153-51
US-09-490-153-51
US-08-199-911-2
US-08-199-911-2
US-08-211-202-111
US-08-211-202-111
US-08-65-202-38
US-09-240-274-39
                                                                                                                                                                                                                                                      ALIGNMENTS
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   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-13
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Best Local Similarity
Matches 13; Conserv
 US-09-383-667-13
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us-10-614-959-13.rai

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US-08-665-202-36

US-08-665-202-36

Sequence 36, Application US/08665202

Patent No. 5977322

GENERAL INFORMATION:

APPLICANT: Marks, James D.

APPLICANT: Schier, Robert

TITLE OF INVENTION: Tumor Antigens

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 98;
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ZIP: 94111-3834

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: FOLDOY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-01N-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: HUNDER: US 00/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: HUNDER: TOWNEY/ANDER: TOWNEY/ANDER/ANDER: TOWNEY/ANDER: TOWNEY/ANDER/ANDER: TOWNEY/ANDER: TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 62; DB 4;
Pred. No. 0.007;
1; Mismatches
                FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY, AGENT INFORMATION:
NAME: HUNTER, TOM
REGISTRATION NUMBER: 02307E-061411
TELECOMMONICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
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REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
US 60/000,250
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

Best Local Similarity 92.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 111 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 SGSSSNIGNNYVS 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SGSTSNIGNNYVS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-315-574-37
    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
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Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Heue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STARET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                         COMPUTER: CALLLLLLLLLCCCONDUTRY: USA
ZIP: 9411-3834
ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATENTIN Release #1.0, Version #1.30
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-UN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 13-UW-1995
FILING DATE: 13-UW-1995
ATTORNEY/AGENT INFORMATION:
NAME: HUNDER: US 60/000,250
FILING DATE: 15-UW-1995
ATTORNEY/AGENT INFORMATION:
NAME: HUNDER: TS-US-1995
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 376-0200
ITELEFAM: (415) 576-0200
ITELEFAM: AND ACTORNATION:
TELEFAM: (415) 576-0200
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LEASTH: DATA ACTERISTICS:
LEASTH: DATA ACTERIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIALE: CALIBORINA
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SGSTSNIGNNYVS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-665-202-37
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Sequence 43, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 597732281 High Affinity Human Antibodies to TITLE OF INVENTION: Tunor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STREET: California

```
STRANDENDESS:

MODELOGY ILLEAR
US-08-665-203-6

OUSTY MARCH
BEST CONSERVATION:

MATCHES 12, CONSERVATION:

MATCHES 12, CONSERVATION:

1 SCSTENICAMYTON:

DD 23 SCSENICAMYTON:

1 SCSTENICAMYTON:

DD 22 SCSENICAMYTON:

APPLICAMYTON:

APPLICAMYTON:
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: HUNTER, TOM

ZIF: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acids

STRANDEDNESS:

```
MOLECULE TYPE: peptide
US-08-665-202-43

Query Match
Best Local Similarity 92.3%; Score 62; DB 2; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0;
Qy 1 SGSTSNIGNNYVS 35

RESULT 7
US-08-983-607-35
; Sequence 35, Application US/08983607
; Patent No. 6140470.
; APPLICANT: Alan Garen
APPLICANT
```

Length 111;

Score 62; DB 2; Le Pred. No. 0.0079; 1; Mismatches 0;

Query Match
Best Local Similarity 92.3%;
Matches 12; Conservative

1 SGSTSNIGNNYVS 13 |||:|||||||| 23 SGSSSNIGNNYVS 35

RESULT 6 US-08-665-202-43

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02307E-061411
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PRICA APPLICATION DATA:
APPLICATION UNBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: HURLEY TOWN
           CLASSITCATION: 2. ....

CLASSITCATION DATA:

APPLICATION NUMBER: US 60/000,238

APPLICATION NUMBER: US 60/000,238

FILING DATE: 14-JUN-1995

PRIOR APPLICATION NUMBER: US 60/000,250

FILING DATE: 15-JUN-1996

APPLICATION NUMBER: US 08/665,202

FILING DATE: 13-JUN-1996

APPLICATION NUMBER: US 08/665,202

FILING DATE: 13-JUN-1996

ATTORNEY-AGENT INFORMATION:

NAME: HUNTER, TOM

REGESTRATION NUMBER: 38,498

REFERENCE/DOCKET NUMBER: 02307E-0614

TELECHONE: (415) 576-0200

TELEPRA: (415) 576-0200

TELEPRA: (415) 576-0200

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 111 amino acids

TYPE: amino acids

TYPE: amino acids

TTYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.9%;
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20-MAY-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-315-574-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Sequence 36, Application US/09315574

Patent No. 6512097

APPLICANT: Marks, James D.
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Heue P.C.
STREET: Four Embarcadero Center, Suite 1100

CITY: San Francisco
STARE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens (melanoma patient immu-ORGANISM: nized with autologous tumor cells) INDIVIDUAL ISOLATE: peripheral blood lymphocytes IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY: DM414 scFv antibodies obtained from LIBRARY: fUSE5 fusion phage construct
                                                                 COMPUTER: IBW PC
OPERATING SYSTEM: MS DOS
SOFTWARE: WORD PLOCESSING
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOREY APPLICATION: 435
APPLICATION NUMBER: BCT/1B96/01032
FILING DATE: JUNE 28, 1996
CLASSIFICATION: 435
ATTORNEY AGENT INDREMATION:
NAME: MALY M. KLIMBKY
REGISTRATION NUMBER: 32423
REFERENCE/POCKET NUMBER: 32423
REFERENCE/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POCKET/POC
           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
DESCRIPTION: polypeptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 SGSSSNIGNNYVS 35
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Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: light chain
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-983-607-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
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Sequence 42, Application US/09315574

Sequence 42, Application US/09315574

Patent No. 6512097

GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tunor Antigens
NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Heue P.C.
STREET: San Francisco
CITY: San Francisco
STREET: California
                                                     Gaps
                                                     ö
Length 111;
                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: California
CCUMTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURSING APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
PRIUM DATA: 14-JUN-1995
PRIUM DATA: 14-JUN-1995
PRIUM DATA: 14-JUN-1995
PRIUM DATA: US 60/000,250
APPLICATION NUMBER: US 60/000,250
APPLICATION NUMBER: US 60/000,250
APPLICATION NUMBER: US 60/000,250
APPLICATION NUMBER: US 60/000,250
Score 62; DB 4;
Pred. No. 0.0079;
                                                       1; Mismatches
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Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Schier, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to TINER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                           Score 62; DB 4; Length 111;
Pred. No. 0.0079;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSER: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/315,574

FILING DATE: 20-MAY-99

CLASSIFICATION NUMBER: US/09/315,574

FILING DATE: 14-JUN-1995

PRIOR APPLICATION NUMBER: US 60/000,238

FILING DATE: 14-JUN-1995

PRIOR APPLICATION NUMBER: US 60/000,250

FILING DATE: 15-JUN-1995

PRIOR APPLICATION NUMBER: US 60/000,250

FILING DATE: 13-JUN-1995

PRIOR APPLICATION NUMBER: US 60/000,250

FILING DATE: 13-JUN-1995

ATPONEY/AGENT INFORMATION:

ANALY AGENT INFORMATION:

ANALY AGENT INFORMATION:

ANALY AGENT INFORMATION:
REGISTRATION NUMBER: 38,498
REPERBENGE/DOCKET NUMBER: 02307E-061411
RELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                             93.9%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPDLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-43
                                                                                                                                                                                                                                                                                                                                                                                                                                              23 SGSSSNIGNNYVS 35
                                                                                                                                                                                                                                                                                                                    Query Match 93.9
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   1 SGSTSNIGNNYVS 13
                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-315-574-42
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US-09-315-574-43
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APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5971322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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    Score 62; DB 4; Length 111;
Pred. No. 0.0079;
1; Mismatches 0; Indels
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Pred. No. 0.008;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Eloppy disk

COMPUTER: Eloppy disk

COMPUTER: Eloppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/665,202

FILING DATE: 13-JUN-1996

CLASSIFICATION NUMBER: US 60/000,238

FILING DATE: 14-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,250

FILING DATE: 15-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: HUNTEY, TOM

RESTRENCE/DOCKET NUMBER: 38,498

REFERENCE/DOCKET NUMBER: 38,498

REFERENCE/DOCKET NUMBER: 3207E-061410

TELECOMMUNICATION INFORMATION:

TELEPRAK: (415) 576-0300

INFORMATION POR SEQ 1D NO: 39:

SEQUINCE CHARACTERISTICS:

FENTALLY OF THE SEQ 1D NO: 39:

FENTALLY OF THE SEQ 1D NO: 39:

FENTALLY OF THE SEQ 1D NO: 39:
                                                                                                                                                                                                                                                    Sequence 39, Application US/08665202
Patent No. 5977322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-08-983-607-31
'Sequence 31, Application US/08983607
'Patent No. 6140470
'GENERAL INFORMATION:
APPLICANT: Alan Garen
Query Match
Best Local Similarity 92.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.9%;
92.3%;
                                                                                          1 SGSTSNIGNNYVS 13
                                                                                                                    23 SGSSSNIGNNYVS 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SGSTSNIGNNYVS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                       RESULT 11
US-08-665-202-39
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NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 112 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SGSTSNIGNNYVS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 92.3
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-7698-18
                                                                           CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                10021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: Human Anti-Tumor Monoclonal
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
ADDRESSEE: Department of Molecular Biophysics
ADDRESSEE: and Blochemistry, Yale University
STREET: Genecticut
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: Gos20-8114
COMPUTER: BADABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: BHB PC
COMPUTER: Mord Processing
COMPUTER: Word Processing
COMPUTER: Mord Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Krinsky
REFERENCE/DOCKET NUMBER: 32423
REFERENCE/DOCKET NUMBER: 32423
REFERENCE/DOCKET NUMBER: 3233
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: DM414 scFv antibodies obtained from LIBRARY: __fUSE5 fusion phage construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 62; DB 3;
Pred. No. 0.008;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 112 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-025-769B-18
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US-09-315-574-39

US-09-315-574-39

Sequence 39, Application US/09315574

Sequence 39, Application US/09315574

BAPLICANT: Marka, James D.

APPLICANT: Marka, James D.

TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to TITLE OF INVENTION: Tumor Antigens

TITLE OF INVENTION: Pumor Antigens

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.

STREET: Four Embarcadero Center, Suite 1100

CITY: San Francisco

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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COMPUTER TREADBLE FORM:

MEDIUM TYPE: Floppy dish
COMPUTER: IBM PC Compadiable
COMPUTER: IBM PC Compadiable
COMPUTER: IBM PC Compadiable
COMPUTER: IBM PC Compadiable
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-199
PRICH DATE: 18-FB-199
PRICH DATE: 18-AUG-195
ATTORNEY AGENT INFORMATION:
NAME: James F. Haley, Jr., EBq.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (2215)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION 1530
PRIOR APPLICATION 1530
PRIOR APPLICATION 1078ER: US 60/000,238
FILING DATE: 14-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 62; DB 3;
Pred. No. 0.008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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us-10-614-959-13.rai

E007 T7:A5:9T C

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PRIOR APPLICATION DATA:

PELIGATION NUMBER: US 60/000,250
PRIOR DATE: 15-JUN-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
FILING DATE: 13-JUN-1996
ATTORNEY AGENT INFORMATION:
NAME: HUNTER, TOM
REGISTRATION NUMBER: 02307E-061411
TELEPHONE: TELEPHONE: 776-0200
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
TELEPHONE: (415) 576-0300
TELEPHONE: (415) 576-0300
TELEPHONE: GHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOSY: linear
MOLECULE TYPE: peptide
US-09-315-574-39
```

Query Match 93.9%; Best Local Similarity 92.3%; Matches 12; Conservative

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COMPUTER READABLE F.C..

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
PRICATION NUMBER: US/09/000
PRICATION NUMBER: BP 95 11 3021.0
PRICATION NUMBER: BP 95 11 3021.0
PRICATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
FELENCAMUNICATION INFORMATION:
FELENCAMUNICATION INFORMATION:
FELENCAMUNICATION INFORMATION:
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                                                                                                                                            Score 62; DB 4; Length 112;
Pred. No. 0.008;
1; Mismatches 0; Indels
TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-490-070A-18
                                                                                                                                                                                                                                                                                                                             Search completed: October 14, 2005, 16:22:02 Job time : 26.5938 secs
                                                                                                                                            Query Match
Best Local Similarity 92.3%;
Matches 12; Conservative
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US-09-490-070A-18

Sequence 18, Application US/09490070A

Patent No. 6656248

GENERAL INFORMATION:

APPLICANT: Knapplik, Achim
Pack, Peter
11ag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)Peptide libraries
NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:
ADDRESSE: Colin G. Sandercock, Esq. c/o Heller Ehrman
STREET: 1666 K Street, N.W., Suite 300

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: PLANCE COMDAILIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 62, DB 4; Length 112;
Pred. No. 0.008;
1; Mismatches 0; Indels
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October 14, 2005, 16:20:10 ; Search time 92.4219 Seconds (without alignments) 58.615 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM protein - protein search, using sw model US-10-614-959-13 66 Title: Perfect score: Run on:

1 SGSTSNIGNNYVS 13 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1859788 seqs, 416717961 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/ Ggn2_6/ptodata/2/pubpa/1000A PUBCOMB.ppp: *
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/ Ggn2_6/ptodata/2/pubpa/1000A PUBCOMB.ppp: *
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/ Ggn2_6/ptodata/2/pubpa/1011A PUBCOMB.ppp: *
/ Ggn2_6/ptodata/2/pubpa/1011A PUBCOMB.ppp: *
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/ Ggn2_6/ptodata/2/pubpa/1010A PUBCOMB.ppp: *
/ Ggn2_6/ptodata/2/pubpa/1010A PUBCOMB.ppp: * Published Applications AA:*

1: /cgnz_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgnz_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

3: /cgnz_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgnz_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

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6: /cgnz_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

7: /cgnz_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

9: /cgnz_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

9: /cgnz_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

9: /cgnz_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		de				
Result No.	Score	Query Match	Query Match Length DB	08	ID	Description
	99	100.0	:		US-09-880-748-1898	ra abat annother
7	99	100.0		15	US-10-293-418-1898	Segmence 1898 An
m	99	100.0	242		US-10-981-692-24	Semience 24 Appl
4	99	100.0			US-10-981-692-40	Semience 40 Appl
2	99	100.0			US-09-880-748-1927	Semience 1927 An
9	99	100.0			US-10-322-673-53	Semience 53 April
7	99	100.0			US-10-293-418-1927	Semience 1927 An
80	99	100.0			US-10-981-692-29	Segrence 1947, Ap
0	99	100.0		18	US-10-981-692-33	Semience 23, Appl
10	99	100.0			US-10-981-465-53	Somionce 53, Appr
11	99	100.0			US-10-981-621-53	Somionee 53, Appl

Sequence 53. Appl	53.	equence 26.	equence 1926.	equence 1926.	equence 3241	equence 31. Ar	equence 36,	equence 191	equence 191	191	equence 191	equence 1440	equence 168;	equence 170		1928	193	144	e 1683	170	1899	1928	equence 1934	46,	equence 88,	27,	37,	44	39,	equence 1419	1618	equence 2049	141
-673-5	1-691-5	0-981-692-2	-09-880-748-192	-293 - 418 - 19	-10-293-418-324	-10-981-692-31	-10-981-692-3	0-748-191	80-748-1	-418-1	-10-2	-09-880-748-1	-09-880-748-1	-09-880-748-1	-09-880-748-1	-09-880-748-1	-09-880-748-1	US-10-293-418-1443	US-10-293-418-1682	7	-10-293-418-1	8-192	-10-293-418-193	-10-935-29	-10-935-290-8	-10-981-692-2	-10-981-69	-11-046-85	-10-981-69	-09-880-748-141	-09-880-748-161	-09-880-748-20	US-10-293-418-1419
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4	243	244	245	245	245	245	245	246	246	246	246	247	247	247	247	247	247	247	247	247	247	247	247	247	247	247	247	247	248	249	249	249	249
100.0	100.0	100.0	100.0		。	00		100.0	8	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		100.0	ë		100.0	100.0
99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99	99
12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36			39			42		44	45

### ALIGNMENTS

```
Sequence 1898, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

JAPPICLANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATENTING VET: 2.0
US-09-880-748-1898
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1 SGSTSNIGNNYVS 13

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Query Match
100.0%; Score 66; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels (

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0; Mismatches
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CTHER INFORMATION: N015D10 scFv

US-10-981-692-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial sequence
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                                                         154 SGSTSNIGNNYVS 166
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Best Local Similarity 100.
Matches 13; Conservative
1 SGSTSNIGNNYVS 13
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US-09-880-748-1927
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| Sequence 24, Application No. US2005016377A1
| Publication No. US2005016377A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B FILE REFERENCE: PF590P1
| CURRENT APPLICATION NUMBER: US/10/981,692
| CURRENT PILING DATE: 2004-11-05 |
| PRIOR PILING DATE: 2005-29 |
| PRIOR PILING DATE: 2002-05-29 |
| PRIOR PILING DATE: 2002-05-30 |
| NUMBER OF SEC ID NOS: 76 |
| SOFTWARE: PatentIn version 3.1 |
| SEC ID NO 24 |
| LEAST SEC ID NO 25 |
| LEAST SEC ID NO 25 |
| LEAST SEC ID NO 24 |
| LEAST SEC ID NO 25 |
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                                                                                                               RESULT 2
US-10-293-418-1898
is Sequence 1898, Application US/10293418
is Publication No. US2003022396A1
is GENERAL INFORMATION:
AFPLICANT: Nuben et al.
TITLE OF INVENTON: Antibodies that Immunospecifically Bind BLyS
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1988
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100.0%; Score 66; DB 18; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels
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US-10-981-692-24
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               153 SGSTSNIGNNYVS 165
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Matches 13; Conservative
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-10-981-692-24
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Sequence 40. Application US/10981692
; Sequence 40. Application No. US2005016377A1
; Publication No. US2005016377A1
; GENERAL INFORMATION:
    APPLICANT Rosen et al.
    TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
    TITLE REFERENCE: PF590P1
    CURRENT APPLICATION NUMBER: US/10/981,692
    CURRENT FILING DATE: 2004-11-05
; PRIOR FILING DATE: 2003-05-29
; PRIOR FILING DATE: 2003-05-29
; PRIOR FILING DATE: 2003-05-30
; WUMBER OF SEQ ID NOS: 76
; SEQ ID NO 40

LENGTH: 242
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; Sequence 1927, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVERNION: Antibodies that Immunospecifically Bind BLyS;
FILE REFERENCE: PFS23
CURRENT FILING DATE: 2001-06-15
; CURRENT FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-01-17
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1927
; LENGTH: 243
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APPLICANT: Rosen et al.

TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
FILE REPERENCE: PF950P1

CURRENT APPLICATION NUMBER: US/10/981,692

PRIOR APPLICATION NUMBER: PCT/US03/16802

PRIOR APPLICATION NUMBER: 60/383,802

PRIOR FILING DATE: 2003-65-29

PRIOR FILING DATE: 2003-65-30

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patentin version 3.1

SEQ ID NO 29

LENGTH. 243
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Sequence 33, Application US/10981692

Publication No. US20050163777A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B

TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B

FILE REFERENCE: PF590P1

CURRENT APPLICATION NUMBER: US/10/981,692

CURRENT FILING DATE: 2003-05-29

PRIOR FILING DATE: 2003-05-29

PRIOR FILING DATE: 2003-05-30

NUMBER OF SEQ ID NOS: 76

SSOTUM PRIOR PALCHALLY NOS: 76

SSOTUM PARE: PatentIn version 3.1

LENGTH: 243
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                                                                     Query Match
100.0%; Score 66; DB 15; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels
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100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels
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100.0%; Score 66; DB 18; Length 243;

Best Local Similarity 100.0%; Pred. No. 0.007;

Matches 13; Conservative 0; Mismatches 0; Indels
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, Sequence 29, Application US/10981692
, Publication No. US20050163777A1
, GENERAL INFORMATION:
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US-10-981-692-29
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OTHER INFORMATION: NO23E01 BCFV

US-10-981-692-33
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ORGANISM: Artificial sequence
PEATURE:
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; ORGANISM: Homo mapiens
US-10-293-418-1927
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RESULT 12
US-10-981-673-53

y Sequence 53, Application US/10981673

publication No. US2000214207A1

GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF585P1D2
CURRENT FILING DATE: 2004-11-05

PRIOR FILING DATE: 2004-11-05

PRIOR FILING DATE: 2004-05-10

PRIOR FILING DATE: 2004-05-10

PRIOR FILING DATE: 2003-05-10

PRIOR FILING DATE: 2003-05-06

PRIOR FILING DATE: 2003-05-06

PRIOR FILING DATE: 2003-05-16

PRIOR FILING DATE: 2002-12-19

PRIOR FILING DATE: 2002-06-04

PRIOR
PRIOR FILING DATE: 2003-08-15
PRIOR PEDLICATION NUMBER: 10/322,673
PRIOR PEDLICATION NUMBER: 60/369,877
PRIOR FILING DATE: 2002-12-19
PRIOR PELING DATE: 2002-04-05
PRIOR PELING DATE: 2002-06-04
PRIOR PILING DATE: 2002-06-06
PRIOR PILING DATE: 2002-07-18
PRIOR PILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/403,370
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/405,737
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-18
PRIOR PELING DATE: 2002-08-15
PRIOR FILING DATE: 2002-01-13
NUMBER OF SEQ ID NOS: 76
LENGTH: 243
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SEQ ID NO 53
LENGTH: 243
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Best Local Similarity 100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels
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US-10-981-673-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
; OTHER INFORMATION: CM085C11 BCFV
US-10-981-621-53
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ORGANISM: Artificial sequence
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; Sequence 53. Application US/10981621
; Publication No. US20050214206A1
; Publication No. US20050214206A1
; GENERAL INFORMATION:
; APPLICAMY: SALCed et al.;
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; TITLE OF INVENTION: Receptors
; FILE REPERENCE: PF565P101
; CURRENT APPLICATION NUMBER: US/10/981,621
; CURRENT FILING DATE: 2004-11-05
; PRIOR FILING DATE: 2004-09-10
; PRIOR FILING DATE: 2004-09-10
; PRIOR FILING DATE: 2004-09-0
; PRIOR FILING DATE: 2004-05-05
; PRIOR FILING DATE: 2003-05-06
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/468,092
                                                                                                                                                                                                                                                                                                                     US-10-981-465-39
US-10-981-465-30
US-10-981-465-30
US-10-981-465-30
US-10-981-465-30
US-10-981-465-30
US-10-981-165-30
US-10-981-10 Wo. US-20050214205A1
GENERAL INFORMATION:

APPLICATOR:
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF8-891
CURRENT APPLICATION NUMBER: US/10/981,465
CURRENT PILING DATE: 2004-09-10
PRIOR PILING DATE: 2004-09-10
PRIOR PAPLICATION NUMBER: 60/468,092
PRIOR APPLICATION NUMBER: 60/468,092
PRIOR FILING DATE: 2003-08-15
PRIOR FILING DATE: 2003-08-16
PRIOR PILING DATE: 2003-08-16
PRIOR PILING DATE: 2002-10-19
PRIOR PILING DATE: 2002-10-19
PRIOR PILING DATE: 2002-10-19
PRIOR PRIUNG DATE: 2002-04-05
PRIOR PILING DATE: 2002-04-0
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100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels (
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US-10-981-465-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 SGSTSNIGNNYVS 167
                                                                         1 SGSTSNIGNNYVS 13
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US-10-981-465-53
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Gaps

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US-10-981-691-53

Sequence 55, Application US/10981691

Sequence 55, Application US/10981691

Sequence 55, Application US/10981691

SEGUENCAL INFORMATION: SECONDER 1

TITLE OF INVENTION: Receptors

FILE REPERENCE: PFS85P1D3

CURRENT APPLICATION NUMBER: US/10/981,691

PRIOR APPLICATION NUMBER: US/40/1090

PRIOR FILING DATE: 2004-01-05

PRIOR APPLICATION NUMBER: PCT/US04/013900

PRIOR PILING DATE: 2004-05-05

PRIOR APPLICATION NUMBER: PCT/US04/013900

PRIOR PILING DATE: 2003-06-15

PRIOR PILING DATE: 2003-06-15

PRIOR PILING DATE: 2003-06-15

PRIOR PILING DATE: 2002-04-05

PRIOR PILING DATE: 2002-01-13

PRIOR PILING DATE: 2002-01-13
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Ouery Match
100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels (
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100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels (

FEATURE: ; OTHER INFORMATION: CM085C11 scFv US-10-981-691-53 TYPE: PRT ORGANISM: Artificial sequence

1 SGSTSNIGNNYVS 13

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155 SGSTSNIGNNYVS 167 US-10-981-692-26 셤

Sequence 26, Application US/10981692
Publication No. US2005016377A1
GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
TITLE OF INVENTION: Antibodies US/10/981,692
CURRENT PILING DATE: 2004-11-05
PRIOR APPLICATION NUMBER: PCT/US03/16802
PRIOR FILING DATE: 2003-05-29
PRIOR FILING DATE: 2003-05-39
PRIOR PILING DATE: 2003-05-30

Gape Sequence 1926, Application US/0980748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT PILING DATE: 2001-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-17

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PeatentIn Ver. 2.0 .. 0 Query Match
100.0%; Score 66; DB 18; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 13; Conservative 0; Mismatches 0; Indels ( ch 100.0%; Score 66; DB 10; Length 245; ll Similarity 100.0%; Pred. No. 0.0071; 13; Conservative 0; Mismatches 0; Indels ( ; NUMBER OF SEQ ID NOS: 76 ; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 26 ; LENGTH: 244 ; TYPE: PRT ; ORGANISM: Artificial sequence ; FEATURE: ; OTHER INFORMATION: NO24D01 scFv US-10-981-692-26 156 SGSTSNIGNNYVS 168 1 SGSTSNIGNNYVS 13 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-880-748-1926 Best Local Similarity US-09-880-748-1926 Query Match g ઠે

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Search completed: October 14, 2005, 17:00:43 Job time : 92.4219 secs

157 SGSTSNIGNNYVS 169

1 SGSTSNIGNNYVS 13

Matches

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2007 77.66.07

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

October 14, 2005, 16:02:59 ; Search time 18.0781 Seconds (without alignments) 69.190 Million cell updates/sec Run on:

US-10-614-959-13 66 1 SGSTSNIGNNYVS 13

Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 283416 seqs, 96216763 residues Searched:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query			SOMETER			
No.	Score	Match	Match Length	DB	ID	Description	no	
Н	62		96	7	836050	To lambda	- ciedo	
~	62	•	111	~	7	-	the de	
е	62		111	~	\$19664	٠,	Chain	
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S	62		232	N	\$25742	٠.	Chain	
9	62	93.9	235	~	805270	•	Chair	
7	59	89.4	130	~	509712	٠.		
œ	57	86.4	130	-	LIHUBL	_	rhain	
σ	99	•	111	~	S47185	-	chain	
10	26	•	131	~	S24321	-	-	
=	55	83.3	111		LIHUNW	Iq lambda	chain	
12	23	•	98	~	S36048	_	chain	
13	53	80.3	111	-	LIHUNG	-		
14	23		129	~	S78058	_	chain	
15	23		130	~	S78057		chain	
91	52		109	7	LIHUEP	_		
11	20		98	~	836046		chain	
18	49	74.2	234	N	825757			
6	48		112	~	C44151			
20		٠.	216	~	A42193	_		
77	45	-	98	~	S36047	~		
22		-	110	~	S36258	_	_	
23	45		112	~	D44151	_	_	
24	45		117	~	S23627	_		
25	45	68.2	233	N	S25752	- ۱	the 40	
56	44	66.7	112	N	A44151	٦,	chain v	
22	44	66.7	112	N	B44151	- ،	y ried?	
28	44	66.7	235	~	S25754	- ۱	cho in	
29	43.5	62.9	235	0	S14675	١,	chain -	

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95 149 2272	2500	233 348 99	107 111 112 414	109 112 217
65.2 65.2 65.2	63.6	63.6 63.6 62.1	62.1 62.1 62.1 63.1	60.6 60.6 60.6
4 4 4 6 6 6 6	~ ~ ~			4 4 4 0 0 0
30 32	3 3 3 5	36 337 38	39 41 42	4 4 4 ພ 4 ሺ

#### ALIGNMENTS

1-Jan-2000	):g312299	0; Сарв
RESULT 1 \$35050 [12] lambda chain - human (fragment) C:Species Homo sapiens (man) C:Species Homo sapiens (man) C:Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000 C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000 C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000 C;Mathiliams, S.C. Submitted to the EMBL Data Library, April 1993 A;Mathiliams, S.C. A;Accession: S36050 A;Accession: S36050 A;Status: preliminary A;Molecule Pype: DNA A;Residues: 1-98 *WIT.	A;Cross-references: EMBL:Z22191; NID:g312298; PIDN:CAA80201.1; PID:g312299 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-91/Domain: immunoglobulin homology <imm></imm>	
) ision 01-Dec-195 y, April 1993	A;Cross-references: EMBL:222191; NID:9312298; PIDN:CAA80201.1; C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-91/Domain: immunoglobulin homology <imm></imm>	Ouery Match 93.9%; Score 62; DB 2; Length 98; Best Local Similarity 92.3%; Pred. No. 0.001; Matches 12; Conservative 1; Mismatches 0; Indels 1 SGSTSNIGNNYVS 13 23 SGSSSNIGNNYVS 35
RESULT 1 \$36050  (i.go lambda chain - human (fragment)  (i.gopecies: Homo sapiens (man)  C:Date: 22-Nov-1993 #sequence_revision 01-Dec-  C:Accession: 356050  submitted to the EMBL Data Library, April 1993  A;Reference number: 336046  A;Sccasion: 336050  A;Sccatus: preliminary  A;Nolecule type: DNA  A;Residues: 1-98 wir,	A;Cross-references: EMBL:Z22191; NID:9312298; C;Superfamily: immunoglobulin V region; immunC;Keywords: heterotetramer; immunoglobulin F;15-91/Domain: immunoglobulin homology <iwm></iwm>	ch 93.9%; 1 Similarity 92.3%; 12; Conservative 1 1 SGSTSNIGNNYVS 13                     23 SGSSSNIGNNYVS 35
RESULT 1 836050 19 lambda chain - human (frag 19 lambda chain - human (frag 19 lambda: Homo sapiens (man) 19 lambe: 22-Nov-1993 #sequence 19 lamba: 336050 19 lamba: 30.5 19 lamba: 10.5 10 lamba: 10.5 1	oss-references perfamily: imm ywords: hetero	Query Match Best Local Similarity 92 Matches 12; Conservative 1 SGSTSNIGNNYVS 1:
RESULT 336050 19 19 19 2000 C; Speam C; Date C; Date C; Ascolo	A;Cr C;Su C;Ke F;15	Ov Ma Oy Db

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RESULT 2
S47009
1g lambda chain VI-J3 region - human
C.Species: Homo sapiens (man)
C.Species: Homo sapiens
C.Species: Homo sapiens
C.Species: Homo sapiens
C.Species: Homo sapiens
C.Species: S47009
R.Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
Submitted to the EMBL Data Library, July 1994
A.Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody binc
A.Species: Dreliminary
A.Accession: S47009
A.Status: preliminary
A.Molecule type: mRNA
A.Status: EMBL: Z35495; NID:G517346; PIDN:CAA84629.1; PID:G517347
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Superfamily: immunoglobulin homology <IMM>
F.15-91/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 111; Best Local Similarity 92.3%; Pred. No. 0.0011; Matches 12; Conservative 1; Mismatches 0; Indels

1 SGSTSNIGNNYVS 13

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Gaps

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Justices Homo sapiens (man)

[1g lambda chain V region - human

[1g lambda chain V region - human

[1g lambda chain V region - human

[2] Species: Homo sapiens (man)

[2] Species: Homo sapiens (man)

[3] Species: 11-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

[3] Species: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 21-Jan-2000

[3] Species: Species: N.C.; Bye, J.M.; Beale, D.; Coadwell, J.

[4] Rithdree Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.

[5] Species: J. 268, 135-140, 1990

[6] A. Highes-Jones, N.C.; Bye, J.M.; MulD:90262535; PMID:2111699

[7] Species: Notecond sequences and three-dimensional modelling of the VH and VL domains of A; Reference number: S09712

[7] Species: Profile: Notecond sequences: Species: Notecond sequences: Species: S
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-references: EMBL:X14583; NID:g33394; PIDN:CAA32725.1; PID:g33395
A; Cross-references: EMBL:X14583; NID:g33394; PIDN:CAA32725.1; PID:g33395
R; Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acid8 Res. 17, 4385, 1989
Nucleic Acid8 Res. 17, 4385, 1989
A; Title: Nucleoride sequences of the cDNAs encoding the V-regions of H- and L-chains of A; Reference number: S04601; MUID:89296497; PMID:2500644
A; Accession: S04601.
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens
Cispecies: Homo sapiens
Cispecies: Solun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
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                   A;Status: preliminary; translation not shown
A;Status: preliminary; translation not shown
A;Residues: 1-232 <CON>
A;Residues: 1-232 <CON>
A;Cross-references: EMBL:X57806; NID:g33709; PIDN:CAA40944.1; PID:g33710
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;147-215/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-130 «KIS2.>
A;Residues: 1-130 «KIS2.>
A;Croser references: EMBL:14583
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin
F;1-20/Domain: signal sequence #status predicted «SIG»
F;21-235/Product: Ig lambda chain #status predicted «MAT»
F;150-218/Domain: immunoglobulin homology «IMM»
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Pred. No. 0.0025;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 232;
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93.9%; Score 62; DB 2; Length 232
Best Local Similarity 92.3%; Pred. No. 0.0025;
Matches 12; Conservative 1; Mismatches 0; Indels
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Best Local Similarity 92.3%;
Matches 12; Conservative 1
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A; Accession: S25742
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Ig lambda chain - human
Ig lambda chain - human
Ig lambda chain - human
C;Species Homo sapiens (man)
C;Dete: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25742
R;Combriato, G; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(Lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam A;Reference number: S16439; MUID:91257162; PMID:1904362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Eulitz, M.; Breuer, M.; Linke, R.P.
Biol. Chem. Hoppe-Seyler 366, 863-870, 1987
A;Title: Is the formation of AL-type amyloid promoted by structural peculiarities of imm
A;Reference number: A29700; MUID:87299022; PMID:3620114
                                                                                                                                                                                                                                                                                               Igliambda chain V region (clone alpha-ph0x15) - human (species: Homo sapiens (man) (c; Species: Homo sapiens (man) (c; Species: Homo sapiens (man) (c; Species: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000 (c; Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000 (c; Date: 22-Jan-1993 #sequence (manual) (manual
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C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Residues: 1-110, W < 0.0N>
A, Residues: 1-110, W < 0.0N>
A, Cross-references: EMBL:X61641; NID:g35458; PIDN:CAA43822.1; PID:g1335271
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Reywords: heterotetramer; immunoglobulin
P;15-91/Domain: immunoglobulin homology < IMM>
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A;Residues: 1-113 <EUL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroteramer; immunoglobulin
P;14-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 113;
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92.3%; Pred. No. 0.0012; Wiemarches 0; Indels
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Pred. No. 0.0011;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, October 1991
A;Reference number: S2444
A;Accession: S2444
A;Molecule type: mRNA
A;Residues: 1-110,'W' <JON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 93.9%;
Best Local Similarity 92.3%;
Matches 12; Conservative :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X61641 R;Jones, P.T.
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nes 12; Conservative
                                      SGSSSNIGNNYVS 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-111 < MAR>
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1 SCSTSNIGNNYVS 13
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Best Local Similarity 84.6
Matches 11; Conservative
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Best Local Similarity 76.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
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[G:Species: Homo sapiens (man)

[G:Species: Homo sapiens (G:Species)

[G:Species: S47185

[G:Species: Homo sapiens (G:Species)

[G:Species: Homo 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: UNIPROT: P06316; GB: X01147; NID: 933335; PIDN: CAA25598.1; PID: 9758087
                                                                                                                                                                                                                                                                               RESULT 8
LiHUBL
Lighanda chain precursor V-I region (BL2) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Dates: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A0196 Hesc. 12, 8407-8414, 1984
A;Title: Modicular cloning of a human immunoglobulin lambda chain variable sequence.
A;Reference number: A01966; MUID:85062823; PMID:6095199
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         Score 59; DB 2; Length 130;
Pred. No. 0.0045;
2; Mismatches 0; Indels
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84.6%; Pred. No. 0.013;
iive 1; Mismatches
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Pred. No. 0.01;
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Ouery Match
Best Local Similarity 84.6%;
Matches 11; Conservative
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                                                                                                                                    1 SGSTSNIGNNYVS 13
                                                                                                                                                                 42 SGTSSNIGNNYVS 54
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Matches 11, Conservative
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Matches 11; Conservative
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C;Accession: S24321
R;Aucouturier, P.; Khamlichi, A.A.; Preud'homme, J.L.; Bauwens, M.; Touchard, G.; Cogne, Biochem. J. 285, 149-152, 1992
Biochem. J. 285, 149-152, 1992
Biochem. J. 286, 149-152, 1992
A;Atitle: Complementary DNA sequence of human amyloidogenic immunoglobulin light-chain pre A;Reference number: S24319; MUID:92344562; PMID:1379039
A;Accession: S24321
A;Accession: S24319; MUID:92344562; PMID:1379039
A;Reference number: S24319; MUID:92344562; PMID:1379039
A;Status: preliminary
A;Molecule type: mRNA
A;Kesidues: 1.131 cANC>
A;Cross-references: EMBL:X64134; NID:g32808; PIDN:CAA45495.1; PID:g32809
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology < IPM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gispecies: Homo sapiens (Mew) - human
Cispecies: Homo sapiens (man)
Cispecies: Appr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
Cispecies: Appr-1954
Ritanger, B.; Steinmetz-Kayne, M.; Hilschmann, N.
Hippec-Seyler's Z. Physiol. Chem. 349, 945-951, 1968
A;Title: The complete amino acid sequence of Bence-Jones protein New (lambda type). Subgray, A;Title: The complete amino acid sequence of Bence-Jones protein
A;Accession: A01964
A;Molecule type: protein
A;Residues: 1-11 < LAN>
A;Residues: 1-11 < LAN>
A;Residues: 1-11 < LAN>
C;Comment: This is a Bence Jones protein.
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A;Gene: GDB:IGLV®
A;Gene: GDB:IGLV®
A;Gene: GDB:IGLV®
A;Gross-references: GDB:I19342; OMIM:147240
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into lan C;Superfamily: immunoglobulin vergion; immunoglobulin homology cimms
C;Keywords: blocked amino end; heterotetramer
F;15-91/Domain: immunoglobulin homology cimms
F;15-91/Domain: immunoglobulin homology cimms
F;17-91/Domain: immunoglobulin homology cimms
F;18-91/Domain: immunoglobulin homology cimms
F;18-91/Domain: immunoglobulin homology cimms
F;18-91/Domain: immunoglobulin homology cimms
F;18-91/Domain: immunoglobulin homology cimms
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S24321
Ig lambda chain precursor - human
G.Species: Homo sapiens (man)
C.Species: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C.Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C.Accession: S24321
C.Accession: S24321
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Ig lambda chain - human (fragment)
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S36048; S36049
R;Williams, S.C.
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Pred. No. 0.015;
1; Mismatches 1; Indels
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84.6%;
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Gaps

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0; Indels

Score 53; DB 2; Pred. No. 0.049; 2; Mismatches

Length 129;

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A;Accession: S21723
A;Molecule type: mRNA
A;Residues: 19-129 - KHAN-
A;Residues: 19-129 - KHAN-
A;Cross-references: EMBL:X54446
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-18/Domain: stopped sequence (fragment) #status predicted <SIG>F;1-129/Product: Ig lambda chain (fragment) #status predicted <MAT>F;3-129/Pommain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                              Query Match 80.3%;
Best Local Similarity 83.3%;
Matches 10; Conservative
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Matches
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A; Gross-references: GDB:I19342; OMIM:147240
A; Cross-references: GDB:I19342; OMIM:147240
A; Cross-references: GDB:I19342; OMIM:147240
A; Gross-references: GDB:I19342; OMIM:147240
A; Gross-references: GDB:I19342; OMIM:147240
C; Complex: An immunoglobulin heterotetramer and IgM, the subunits associate into la C; Superfamily: immunoglobulin to region; immunoglobulin homology
C; Keywords: blocked amino end; heterotetramer
F;15-91/Domain: immunoglobulin homology < IMM'
F;15-91/Domain: immunoglobulin homology < IMM'
F;17-91/Hodified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu
F;22-89/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-129 < HAR>
A; Residues: 1-129 < HAR>
A; Cross-references: EMBL:XS4446; NID:g37923; PIDN:CAA38313.1; PID:g930121
A; Cross-references: EMBL:XS4446; NID:g37923; PIDN:CAA38313.1; PID:g930121
B; Haranton Coldfarb, I.S.; Ikemateu, H.; Burastero, S.E.; Wilder, R.L.; Notkins Int. Immunol. 3, 865-875, 1991
A; Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cispecies: Homo sapienë (man)
Cispecies: Homo sapienë (man)
Cispecies: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
Cispace: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
Cispacesion: A01965
R;Kametani, F.; Takayasu, T.; Suzuki, S.; Shinoda, T.; Okuyama, T.; Shimizu, A.
R;Kametani, F.; Takayasu, T.; Suzuki, S.; Shinoda, T.; Okuyama, T.; Shimizu, A.
A;Title: Comparative studies on the structure of the light chains of human immunoglobuli
A;Reference number: A91970; MUID:83186114; PMID:6404900
                                                                                                          A;Status: Drainfinary
A;Retus: preliminary
A;Residues: 1-98 <WIL>
A;Residues: 1-98 <WIL>
A;Residues: 1-98 <WIL>
A;Residues: 1-98 <WIL>
C;Superferences: EMBL:Z22189; NID:g312294; PIDN:CAA80199.1; PID:g312295; EMBL:Z22190
C;Superferily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-91/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                             Length 98
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A;Reference number: S23716; MUID:92031262; PMID:1718404
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Pred. No. 0.037;
2; Mismatches
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                          to the EMBL Data Library, April 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 1-111 <KAM>
A;Cross-references: UNIPROT:P01702
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Best Local Similarity 83.3%;
Matches 10; Conservative
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Best Local Similarity 76.9
Matches 10; Conservative
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                                                        A; Reference number: S36046
A; Accession: S36048
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S78058
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A; Molecule type: mRNA
A;Regidues: 1-130 <hR>>
A;Cross-references: EMBL:X54438; NID:g37920; PIDN:CAA38307.1; PID:g37921
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins, Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and hJ
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Ig lambda chain precursor V-J region (clone mAB 61VL) - human (fragment) C;Species: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Decies: Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999 C;Accession: S?8057; S23722 R;Harindranath, N...
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-130/Product: Ig lambda chain (fragment) #status predicted <MAT>
F;34-110/Domain: immunoglobulin homology <IMM>
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83.3%; Pred. No. 0.049;
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                                                                                                                                                                  submitted to the EMBL Data Library, August 1990 A; Reference number: S78051 A; Accession: S78057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: October 14, 2005, 16:23:38 Job time : 18.0781 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Molecule type: mRNA
A, Residues: 20-130 <HAW>
A, Cross-references: EMBL:X54438
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S 16:39:22 Z005
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October 14, 2005, 15:51:44; Search time 66.5312 Seconds (without alignments) 76.932 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM protein - protein search, using sw model Title: Perfect score: Sequence: Run on:

US-10-614-959-13 66 1 SGSTSNIGNNYVS 13

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ption	P06316 homo sapien	рошоц	homo	homo	homo	homo	homo	homo	homod	bomod 4	homo	Q871h3 vibrio para		_		Q9w4m4 drosophila		Q17329 caenorhabdi				042275 electrophor		P06887 homo sapien	Q9vrw7 drosophila	_	Q68vs3 rickettsia	_	80		
SUMMERIES	ΙD	LV1G HUMAN	QBIZDB	Q8TE63	LV1C_HUMAN	Q96S <u>B</u> 0	LV1D HUMAN	LV1 I HUMAN	66NI9Q	Q8NEJ1	Q6DHW4	QGGMW6	Q87LH3	Q78CJ5	Q8JRX2	6NZMLO	Q9W4M4	YL52_CAEEL	017329	096223	Q6GMV7	Q971XX3	ACES_ELEEL	LV6D_HUMAN	LV1H HUMAN	Q9VRW7	HEM1_RICPR	Q68VS3	Q6BK59	Q7RRT8	Q95SG4	Q9W117
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	Query Match Length	130	101	110	111	108	111	109	235	236	237	235	221	326	441	1170	1357	2186	2272	2500	236	348	633	111	112	388	414	414	847	928	1272	1272
٠,	Match	86.4	84.8	83.3	83.3	80.3	80.3	78.8	78.8	77.3	74.2	68.2	66.7	66.7	66.7	65.2	65.2	65.2	65.2	65.2	63.6	63.6	63.6	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1
	Score	57	99	22	. 22	23	23	25	52	21	49	45	44	44	44	43	43	43	43	43	42	42	42	41	41	41	41	41	41	41	41	41
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2 drosophila 0 drosophila 0 plasmodium 8 homo sapien 0 homo sapien 2 photorhabdu 1 caenorhabdi 1 ycopersico 5 escherichia 2 arabidopsis 6 francisella 9 neurospora 7 anopheles 9
081180 081180 081150 081150 081150 084150 08412 09412 09412 09412 07253 07253
QBI1E2 QBI1A0 QBI1A0 QBI150 LV1F_HUMAN LV1B_HUMAN QBGFB2 QFFB2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QBF1E2 QB
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0.0000000000000000000000000000000000000
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ALIGNMENTS

RESULT 1

LVIG HUMAN ID 1401G HUMAN TO 1-JAN-1988 (Rel. 06, Created) DT 01-JAN-1988 (Rel. 06, Last sequence update) DE 15-JUL-1999 (Rel. 38, Last annotation update) CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NCBI TaxiD=9606; NCBI TaxiD=9606;	1147; CAA25598 1966; LIHUBL. 017037; 7FAB. 0003823; F:anti 0006955; P:anti 0006955; P:anti 0006965; P:anti 0006965; P:anti 00069666; P:anti 000696666; P:anti 00069666; P:anti 00069666; P:anti 000696666; P:anti 00069666; P:anti 00069666; P:anti 000696666; P:anti 000696666; P:anti 000696666; P:anti 000696666; P:anti 0006966666; P:anti 0006966666; P:anti 0006966666; P:anti 0006966666666; P
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1 SGSTSNIGNNYVS 13

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Query Match 86.4%; Score 57; DB 1; Length 130; Best Local Similarity 84.6%; Pred. No. 0.069; Matches 11; Conservative 2; Mismatches 0; Indels

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Gaps

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23 SGTSSNIGNNFVS 35
1 SGSTSNIGNNYVS 13
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P01701;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                 Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
MEDLINE-95007525; PubMed-7923137;
Hall B.L., Murray J.H., Haspel M.V., Kobrin B.J.;
"Egtablishment, molecular rescue, and expression of 123AV16-1, a tumor-reactive human monoclonal antibody.";
cancer Res. 54:5778-5185(1994).
EMBL; L33985; AAL68704.1;
HSSP; P01703; 7FAB.
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84.6%; Pred. No. 0.079;
tive 1; Mismatches 1; Indels
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                                                                      0; Indels
                                                                                                                                                     [1] ^- SEQUENCE FROM N.A. SEQUENCE FROM N.A. Jung Y.-Y.; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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NON TER 101 101
SEQUENCE 101 AA; 10374 MW; 1506C2D9AACBA793 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            01-07N-2002 (TrEMBLrel. 21, Created)
01-07N-2002 (TrEMBLrel. 21, Last sequence update)
01-07T-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
mmunglobulin light chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                          110 AA
                                                   101 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                   PRT;
                                                                                                                                                                                       EMBL, AY145444; AAN64328.1; -..
EMBL, P01703; 7FAB.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR007110; Ig-like.
Interpro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                     1 SGSTSNIGNNYVS 13
                                                                                                                                                                                                                                                                                                                                                 113 SGSSSNIGKNYVS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
                                                                                                                                                                                                                                                                                                     Local Similarity 84.6
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                    PRELIMINARY;
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   42 SGSSSNIGNDYVS
                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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Matches 10, Conserv
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SEQUENCE
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                                                   Q81ZD8
                                                                                                                                                                                                                                                                                                                                                                                                           Q8TE63
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Q8TE63
                               RESULT 2
Q81ZD8
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Langer By Steinmetz-Kayne M. Hilschmann N.;
Langer By Steinmetz-Kayne M. Hilschmann N.;
Langer By Steinmetz-Kayne M. Hilschmann N.;
The complete antho acid sequence of Bence Jones protein New (lambda-type). Subgroups in the variable part of immunoglobulin L-chains of the lambda-type."

The lambda-type."
The lambda-type."
This is a Bence-Jones protein.
The MISCELLANEOUS: This is a Bence-Jones protein.
This A01964; LIHUNW.
RPSP: P01703; 7FAB.
GO; GO:000576; C:extracellular; NAS.
GO; GO:0005925; P:antigen binding; NAS.
R GO; GO:0006955; P:immune response; NAS.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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NCBI_TaxID=9606;
                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0965B0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98375893; PubMed-9712075; Adderson B.E., Shikhman A.R., Ward K.E., Cunningham M.W.; Adderson B.E., Shikhman A.R., Warde monoclonal antibodies from "Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis; human anti-N-acety1glucosamine/anti-myosin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyrrolidone carboxylic acid By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 111
111 Aa; 11453 MW; AAECBCA3C49F2AD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ig lambda chain V.I region NEW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 AA.
111 AA.
PRT;
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STANDARD;
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EXPLORENT SECTION OF S
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 104 N-Innked (GlcNAc. ..).
22 89 By similarity.
109 109 MW, 556A313E24D5AC73 CRC64;
                                        01-JAN-1988 (Rel. 06, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) 1 lambda chain V-I region EPS. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SGSTSNIGNNYV 12
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Best Local Similarity
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DISULFID
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SEQUENCE
                                                                                                                                                                                                                                                                                 SEQUENCE.
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Q6IN99
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J. Blochem. 93:421-429(1983).
J. Blochem. 93:421-429(1983).
J. Blochem. 93:421-429(1983).
J. SIMILARITY: Contains 1 immunoglobulin-like domain.
PIS, A01965; LIHUNG.
PIS, A01965; LIHUNG.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR00110; Ig-like.
InterPro; IPR00110; Ig-v.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE=81186114; PubMed=6404900;
Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
Shimizu A.;
                                                                                                                                                                                                                                                                                                                                                         80.3%; Score 53; DB 2; Length 108;
83.3%; Pred. No. 0.28;
Live 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig-like.
Pyrrolidone carboxylic acid
By similarity.
                                                                                                                                                                                                                                                                     NON TER 1 1
SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Ig lambda chain V-I region NIG-64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                  antibody V region genes.";
J. Immunol. 16:2020-2031(1998).
EMBL; U96394; AAB68783.1;
PDB; IKU4; Model; L=1.108.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003596; Ig-v.
SMART; SW00406; IGV.
PROSITE; PS50835; IG_LIKE; 1.
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Best Local Similarity 76.9
                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 83.3
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P01702;
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LIVID HUMAN

AC P017024

DT 21-JUL.

DT 21-JUL.

DT 05-JUL.

DT 05-JUL.

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RP SEQUENK

RA KAMELINI

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78.8%; Score 52; DB 1; Length 109; 83.3%; Pred. No. 0.42; tive 1; Mismatches 1; Indels

Conservative

Ig-like.
N-linked (GlcNAc. . .).
By similarity.

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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Straubberg R.L., Collina F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                               Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                        Q6IN99 PRELIMINARY; PRT; 235 AA.
Q6IN99;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
IGLC2 protein.
Name=IGLC2;
23 SGSSSNIGKNYV 34
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=9606;
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109 AA.

INII HUMAN ID LV11 HUMAN STANDARD; AC P06888; DT 01-JAN-1988 (Rel. 06, Created)

23 SGSSSNIGDNFVS 35

1 SGSTSNIGNNYVS 13

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Lung;
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QEDHW4
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Nodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., A Jones S.J., Marra M.A.;

and mouse CDNA sequences.";
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., C., Krimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                      InterPro; IPR001359; Ig.
InterPro; IPR001359; Ig-like.
InterPro; IPR003006; Ig-like.
InterPro; IPR003006; Ig-mHC.
InterPro; IPR003596; Ig-v.
Pfam; PPG07654; Cl-set; I.
SWART; SW00407; IG-l.
SWART; SW00407; IG-l.
SWART; SW00407; IG-l.
PR051TE; PS50835; IG LIKE; 2.
PR051TE; PS50835; IG LIKE; 2.
PR051TE; PS0939; IG WHC; UNKNOWN 1.
SEQUENCE 235 AA; Z4888 MW; 90C95D5E87A6BCC1 CRC64;
                                                                                                                                                                     Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO72392; AAH72392.1; -.
HSSP; P01042; 1AQK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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nes 10; Conservative
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SEQUENCE FROM N.A.
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Table Statement From N. A.

Table Statement B Cells;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ra Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ratanner R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Ra Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,

Ra Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,

Ratchenko L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

Raplecon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raplecon M., J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., Loquellano N.A., Pecers G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Richards S., Worley W.C., Sodergren B.J., Lu X., Gibbs R.A.,

Rahesjey R.W., Touchman M., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rayminski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Ryayminski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Radminse Chuk Berniannen ""

H. "Generation and initial analysis of more than 15,000 full-length human men and mouse chara.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.3%; Score 51; DB 2; Length 236; 83.3%; Pred. No. 1.3; 1.4ve 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC075843; AAH75843.1; -.
                                                                                                                                                                Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BC030984; AAH30984.1; -.
HSSP; P01703; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 236 AA; 25024 MW; 1703B77942630E08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                INCEPPO IPROOFILD; IG-like.
INCEPPO IPROOFILD; IG-like.
INCEPPO IPROOFICE; IG-C1.
INCEPPO IPROOFICE; IG-MHC.
INCEPPO IPROOFICE; IG-MHC.
PEAM; PFO7654; C1-8et; I.
PROSITE; PSC60256; IG-LIKE; I.
PROSITE; PSC60256; IG-LIKE; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003599; IG.
InterPro; IPR007110; IG-like.
InterPro; IPR003597; IG-C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sednences.
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les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SGSTSNIGNNYV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Primary B-Cells;
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                                                                                          SEQUENCE FROM N.A.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
IPEm; PP00454; Cl.set; I.
Pfam; PP00454; Cl.set; I.
SMART; SM00409; IG; 2.
SMART; SM00400; IG; 2.
SMART; SM00406; IGV; 1.
SMART; SM00406; IGWHC; UNKNOWN_I.
SMOSITE; PS00220; IGWHC; UNKNOWN_I.
HYPOCHETICAL protein_S17 AA; 25108 MW; 6814170F7E784825 CRC64;

Score 49; DB 2; Length 237; Pred. No. 3; 1; Mismatches 1; Indels Query Match 74.2%; Best Local Similarity 83.3%; Matches 10; Conservative

1 SGSTSNIGNNYV 12 ઠે 셤

42 SGSSSNIGINYV 53

05-JUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) PRELIMINARY; QGGMM6; **DEGMW6** RESULT 11
OGGMW
AC
OGGMW
AC
OGGMW
DT
OS-JT
OS-JT
DT
OS-JT
OS-JT
DT

Hypothetical protein. Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;

SEQUENCE FROM N.A.

YESUBE-Primary B-Cells;

X Facuster, R. W. Felingold E. A., Grouse L. H., Derge J. G.,

X Strausberg R. L., Felingold E. A., Grouse L. H., Derge J. G.,

X Rausberg R. L., Felingold E. A., Grouse L. H., Derge J. G.,

X Rausberg R. L., Felingold E. A., Grouse L. H., Derge J. G.,

X Altschul S. P., Zeeberg B. Buetow K. H., Schaefer C. F., Bhat N. K.,

Hopkins R. P., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,

A platchenko L., Marusina K., Farmer A.A., Rubin G. M., Hong L.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T. L., Scheetz T. E.,

Rapieton M. J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S. S., Loquellano N.A., Peters G. J., Abramson R. D., Mullahy S. J.,

Rosak S.A., McKaran P. J., McKernan K. J., Malek J. A., Gunaratne P. H.,

X Richards S., Worley K.C., Hale S., Garcia A.M., Gay L. J., Hulyk S. W.,

Yillalon D. K., Muzny D. M., Sodergren B. J., Lu X., Gibbs R. A.,

X Halton D. K., Marny D. M., Sodergren B. J., Lu X., Gibbs R. A.,

X Halton D. K., Marny D. M., Green B. D., Dickson M. C.,

Rabesley R. W., Touchman J. W., Green B. D., Dickson M. C.,

Rodriguez A.C., Grimwood J. W., Green B. D., Dickson M. C.,

Rodriguez A.C., Grimwood J. W., Green B. D., Dickson M. C.,

Rodriguez A.C., Marra M. A.,

Jones S.J., Myers R. M.,

Jones CDNA sequences ",

PR. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

| SEQUENCE FROM N.A. | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 | 1.25 |

PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
Hypothetical protein.
SEQUENCE 235 AA; 24803 MW; 058B05F61118F1B8 CRC64;

ö 68.2%; Score 45; DB 2; Length 235; 69.2%; Pred. No. 14; tive 3; Mismatches 1; Indela Query Match Best Local Similarity 69.2° Matches 9, Conservative

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Gaps

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RESULT 12 Q87LH3 ID Q87LH

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221 AA PRELIMINARY; Q871.H3

01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUNA-2004 (TrEMBLrel. 26, Last annotation update)
Putative short-chain dehydrogenase.
OrderedLocusNames=VP2639;

Vibrio parahaemolyticus. Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.

SEQUENCE FROM N.A.

STRAIN=KIMD 2210633 / Serotype O3:K6;

MEDLINE=22508454; PubMed=12650739; DOI=10.1016/S0140-6736(03)12659-1;

Makino K., Oshima M., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakamo M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae.";

Lancet 361:743-749(2003).

GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR002198; ADH short.
Pfam; PF00106; adh short; 1.
PRINTS; PR00001; GDHRDH.

221 AA; 23803 MW; D545E953C9AB3A2F CRC64;

Score 44, DB 2; Length 221; Pred. No. 20; 2; Mismatches 2; Indels 66.78; Local Similarity 66.7 108 8; Conservative Query Match

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RESULT 13 Q7SCJ5

PRELIMINARY;

Created) Last sequence update) Last annotation update) Q7SCJ5; 01-MRR-2004 (TrEMBLrel. 26, C; 01-MRR-2004 (TrEMBLrel. 26, L; 01-MRR-2004 (TrEMBLrel. 26, L; Hypothetical protein. Name=NCU00836.1;

Neurospora crassa. Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

SEQUENCE FROM N.A. STRAIN=OR74A; Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,

PRT; 1170 AA

PRELIMINARY;

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STRAIN=PA14;
PubMed=14983043; DOI=10.1073/pnas.0304622101;
PubMed=14983043; DOI=10.1073/pnas.0304622101;
He J., Baldini R.L., Deziel E., Saucier M., Zhang Q., Liberati N.T.,
Lee D., Urbach J., Goodman H.M., Rahme L.G.;
"The broad host range pathogen Pseudomonas aeruginosa strain PA14
carries two pathogenicity islands harboring plant and animal virulence
                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 101:2530-2535(2004).
EMBL; AY273871; AAP81276.1; -
InterPro; IPR008707; NeisBerria.PilC.
Pfam; PPC5567; NeisBerria PilC; 1.
SEQUENCE 1170 AA; 128118 MW; 9F4CDF6D681B62F3 CRC64;
                                                                                                (TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 70.v.
7, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GSTSNIGNNY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=287;
                                                                                                     01-OCT-2003 (
01-OCT-2003 (
01-MAR-2004 (
PilY1.
                                                                                                                                                                                                                                                                                        Name=pilY1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes."
              Q7WZN9
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DA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Qui D., Ianakiev P., Pedersen D., Nielsen M., Washburne M., Schliter J., Endrizzi M., A Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schlite U., A Schle G.O., Jedd G., Mawes W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S., A Ramal M., Kamvysselis M., Maucell E., Bielke C., Rudd S., Frishman D., A Krystofova S., Rammssen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C., Macino G., Catcheside D., Li W., Fratt R.J., Osmani S.A., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Fretteg M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B., Trhe Genome Sequence of the Filamentous Fungus Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
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2; Indels

2; Mismatches

Score 44; DB 2; Length 441; Pred. No. 41;

66.7%;

Ouery Match
Best Local Similarity 66...
8; Conservative

264 SCNLFNIGNNYL 275

RESULT 15

Q7WZN9

1 SGSTSNIGNNYV 12

δ g

441 AA; 51639 MW; DC7B3982232E3550 CRC64;

SEQUENCE

Phthorimaea operculella granulovirus. Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus. NCBI_TaxID=192884;

01-OCT-2002 (TrEMBLrel. 22, Created) 01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-UNN-2003 (TrEMBLrel. 24, Last annotation update) Late expression factor 4.

441 AA

PRT;

PRELIMINARY;

DBJRX2; Q8JRX2

RESULT 14

311 SGSTCKVGNDYYS 323

1 SGSTSNIGNNYVS 13

ð 원 Croizier L., Taha A., Croizier G., Lopez Ferber M.; Submitted (App. 2002) to the EMBL/GenBank/DDBJ databases. EMBL, AF499596; AAM70285.1; GO, GO:0030528; F:transcription regulator activity; IEA. GO, GO:004449; P:regulation of transcription; IEA. Interbro; IRR007790; LEF-4.

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Gaps

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65.2%; Score 43; DB 2; Length 1170; 70.0%; Pred. No. 1.6e+02; Live 2; Mismatches 1; Indels

COOZ ZZ:KEIGT C

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GenCore version 5.1.6
        Copyright
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Run on:		October 14,	2005,	October 14, 2005, 15:51:19; Search time 53.8125 Seconds (without alignments) 50.310 Million cell updates/sec
Perfect score:	score:	US-10-614-959-14 35	29-14	

1 DVSKRPS 7 Scoring table: Sequence:

2105692 seqs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp2190s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2003bs:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aav79072 Anti-fact		•		Ant	Aau02612 Anti-adip	7 Ant:	σ	_	Aau02542 Anti-adin				Adq42838 BCFv Ab12		Human	Human	Single	Human E	Single	Neuroki	. ~		•	, don't	,
SUMMARIES	H	AAY79072	ADJ80338	AAU02544	AAY96060	AAU02558	AAU02612	AAU02627	AAU02629	AAW19883	AAU02542	AAU02551	AAU02585	ADK17416	ADG42838	ABM85072	ABM85084	ABP45887	ADG96714	ABP46044	ADG96871	ADG34301	ADG34317	ABP45916	ADG96743	ADG34310	
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	Score	35	35	32	35	32	9.0	32	32	35	35	35	32	35	32	32	35	35	32	32	32	35	32	35	35	35	
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35	32		S		S	S	35	35	32	32	35	35	32	35	35	32	32	32	32
26	27		29	30	31	32	33	34	35	36	37	38	39	40	41	42	.43	44	45

ALIGNMENTS

AAY79072 standard; peptide; 7 AA. RESULT 1 AAY79072

AAY79072;

(first entry) 12-JUN-2000 Anti-factor IX/IXa antibody L chain V domain CDR2 amino acid sequence

Complementarity determining region 2; CDR2; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; light chain; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metasteas; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC.

Homo sapiens.

WO200012562-A1.

09-MAR-2000

99WO-US019453. 26-AUG-1999; 28-AUG-1998;

98US-0098233P. 99US-0122767P. 03-MAR-1999;

(GETH) GENENTECH INC.

Kirchhofer D; Judice JK, Навв РЕ, Devaux B, Eaton DL, Adama CW, Suggett S;

WPI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction. CCCCCX8X444X6X11XX6XX3X6X6X6X6X6X6X6X6X6X6X6X6X6X6

Claim 8; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 2 (CDR2) of the light chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXa is a vitamin K dependent plasma serine procease that participates in the blood coaqulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

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the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary artery bypassy (FTCA), stroke, tumour growth, invasion or metaersais, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
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Sequence 7 AA;

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Length 7;
                       0; Indels
       Score 35; DB 3; L
Pred. No. 1.8e+06;
0; Mismatches 0;
         100.0%;
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Best Local Similarity luv.
7; Conservative
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DVSKRPS 7

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ADJ80338 standard; protein; 99 AA.
           06-MAY-2004 (first entry)
                      Homo sapiens
       ADJ80338;
RESULT 2
 ADJ80338
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hybrid antibody; antibody; framework region; homology; immunogenicity. Vlambda gene locus antibody amino acid sequence #7.

402003048321-A2

12-JUN-2003

03-DEC-2002; 2002WO-US038450

03-DEC-2001; 2001US-0336591P

(ALEX-) ALEXION PHARM INC

Wu D; Rother R,

WPI; 2003-513753/48.

Producing a hybrid antibody or hybrid antibody fragment by operatively linking the selected framework sequences to one or more complementarity determining regions of the initial antibody.

Disclosure; SEQ ID NO 98; 77pp; English.

The invention relates to a method of producing a hybrid antibody or hybrid antibody fragment by: (i) providing an initial antibody having pecificity for a target; (ii) determining the sequence of a variable region of the initial antibody; (iii) selecting a first component of the variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the sequence of the first component to sequence contained in a reference at antibody sequences or antibody fragment sequences from a target species; (v) selecting a sequence from an antibody in the database of the demonstrates a high degree of homology to the first component; (vi) selecting a second component of the variable region which is different than the first component, the second component selected from the group consisting of FR1, FR2, FR3 and FR4; (vi) comparing the sequence of the second component to sequences contained in a reference database of second component to sequences contained in a reference database of antibody sequences or antibody fragment sequences from the target species; (vii) selecting a sequence from the database which demonstrates a high degree of homology to the second component and which is from a different antibody than the selected antibody; and (ix) operatively linking the

ANU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain. light chain,
and heavy chain complementarity determining regions (CDR) of the
cinvention. The antibodies can be used in the treatment of obesity and
charged at the antibodies can be used to deliver drugs or
charged directly to the far mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
cectable label such as radiolabel, fluorescent or chemical group and
used in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies

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selected framework sequences to one or more complementarity determining regions (CDRs) of the initial antibody to produce a hybrid antibody or hybrid antibody fragment. The method is useful for producing a hybrid antibody or hybrid antibody fragment (claimed). The antibody and fragments are useful for therapeutic and diagnostic purposes. The method uses entire framework regions from a single antibody variable heavy or variable light chain to receive the CDRs. This produces antibodies that are highly homologous and exhibit reduced immunogenicity while maintaining an optimum binding profile. This sequence represents the amino acid sequence of an antibody from the Vlambda gene locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
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                                                                                                                                                                                                                                                                                                                                              AAU02544 standard; protein; 109 AA.
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                   52 DVSKRPS
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                                                                                                                                                             Sequence 99 AA;
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for different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
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|Jabel= CDRII
|note= "complementarity determining region II"
                                                                                                                                                                                                                                                                                  "complementarity determining region I"
                                         / Match 100.0%; Score 35; DB 4; Length 109; Local Similarity 100.0%; Pred. No. 6; Indels 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                   Human anti-DAF antibody LU30 light chain variable region.
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:e= "hypervariable loop residues"
                                                                                                                                                                                                                                                                                        .35
ce= "hypervariable loop region"
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                                                                                                                                  AAY96060 standard; protein; 110 AA.
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/label= CDRI
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                                                                                                                                                                    05-DEC-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carter PJ, Ridgway JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC
                                                                                    51 DVSKRPS 57
                                                                          1 DVSKRPS 7
                         Sequence 109 AA;
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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obserty and obserty related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the Claim 1; Page 128-129; 182pp; English. Making antibodies (e.g. anti-decay accelerating factor antibody) for diagnosing or treating e.g. lung cancer comprises identifying an antigen that is differentially expressed on the surface of two or more distinct cell populations. The present sequence is that of the light chain variable region (VL) of the anti-decay accelerating factor (DAF) human antibody LU30. The VH region is given in AAY06063. LU30 has a binding affinity (Kd) for DAF of about 13 nM. It was produced using a novel method for making antibodies which can be used for cancer diagnosis or therapy. The method comprises:

Disclosure; Fig SA; 52pp; English.

WPI; 2000-594169/56.

diseases.

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120 (a) binding an antibody phage from a naive antibody phage library to a live cancer cell; (b) selecting an antibody phage or antibody which binds selectively to the live cancer cell; and (c) identifying an antigen to which the antibody phage or antibody binds. To obtain LU30, a human scFv library was used to search for tumour-associated antigens by panning the lum and adenocarcinoma cell line 1264, and counter-selecting with a nontumour bronchial epithelial cell line, BEAS-2B. The invention also chescribes a method for identifying an antigen which is differentially expressed on the surface of 2 or more distinct cell populations. The antice of the configuration comprising the antibody, is useful for diagnosis or therating lung cancer, the santibody is useful for diagnosing or treating lung cancer, e.g. small-cell lung cancer, non-small cell lung cancer, large cell lung carcinoma, lung cancer, non-small cell lung carcinoma (all claimed)
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                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.
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Best Local Similarity 100.00
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N-PSDB; AAS03458.
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                                                                                                                                                                                                                                Sequence 110 AA;
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Gaps

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100.0%; Score 35; DB 4; Length 110; 100.0%; Pred. No. 6.1; cive 0; Mismatches 0; Indel8

7; Conservative

Matches

Query Match Best Local Similarity

DVSKRPS 57

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DVSKRPS 7

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presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases.
                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                   Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                              Anti-adipocyte monoclonal antibody light chain, FAT 99.
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                                                                                                                                                                                                                                           AAU02612 standard; protein; 110 AA
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N-PSDB; AAS03512.
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                                                                                    Sequence 110 AA;
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Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.

Anti-adipocyte monoclonal antibody light chain, FAT 112.

29-AUG-2001 (first entry)

AAU02627;

AAU02627 standard; protein; 110 AA.

RESULT 7 AAU02627

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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
sequences of anti-adipocyte monoclonal antibody heavy chain.

Invention. The antibodies can be used in the treatment of obesity and
chesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the far mass of an obess patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
of complement mediated lysis. The antibodies may be labeled with a
detectable label such as radiolabel, fluorescent or chemical group and
cused in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
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100.0%; Pred. No. 6.1;
ive 0; Mismatches
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Matches 7; Conservative
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ANU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
light chain,
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Sequence 110 AA;

Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related

Claim 1, Page 172; 182pp; English.

diseases

(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

99US-0158812P

12-OCT-1999;

11-OCT-2000; 2000WO-GB003900.

40200127279-A1. Homo sapiens.

19-APR-2001.

Edwards BM, Main SH, Vaughan TJ;

WPI; 2001-282031/29

N-PSDB; AAS03527

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2007 77:88:0T C
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(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
        .AAU02629 standard; protein; 110 AA.
                                                                                                          Edwards BM, Main SH, Vaughan TJ;
                                                                                11-OCT-2000; 2000WO-GB003900
                                                                                         12-OCT-1999; 99US-0158812P
                        29-AUG-2001 (first entry)
                                                                                                                  WPI; 2001-282031/29.
N-PSDB; AAS03529.
                                                               WO200127279-A1.
                                                       Ното варіеля
                                                                        19-APR-2001
                AAU02629;
                                                                                                                                        diseases
   RESULT 8
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Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related

Claim 1; Page 173; 182pp; English.

AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
cobesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
complement mediated lysis. The antibodies e.g. to determine the
complement mediated lysis in human subjects e.g. to determine the
cused in methods of diagnosis in human subjects e.g. to determine the
consence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intraabdominal fat associated with heart disease

Sequence 110 AA;

Gaps ô 100.0%; Score 35; DB 4; Length 110; 100.0%; Pred. No. 6.1; ive 0; Mismatches 0; Indels Query Match 100. Best Local Similarity 100. Matches 7; Conservative

1 DVSKRPS 7

DVSKRPS 57

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AAW19883 standard; protein; 111 AA. AAW19883; RESULT 9
AAW19883
ID AAW1:
XX
AC AAW1:
XX

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Carcinoembryonic antigen; CEA; human; antibody; scFv; tumour marker;
lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.
             CEA-specific antibody CEA1, CEA2, CEA3 VL sequence.
                                                                                                                                                                                                        (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                     96GB-00010824.
                                                                                                                                                                                                                     Osbourn JK, Allen DJ,
                                                Homo sapiens
                                                                                                                                      WO9720932-A1
                                                                                                                                                                 09-DEC-1996;
                                                                                                                                                                              07-DEC-1995;
                                                                                                                                                                                           11-OCT-1996;
                                                                                                                                                   12-JUN-1997
                                                                   Region
                                                                                        Region
                                                                                                            Region
Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
                                                                Anti-adipocyte monoclonal antibody light chain, FAT 113.
```

90. .100 //label= CDR3 /note= "complementarity determining region 3"

96WO-GB003043 95GB-00025004

50. .56 /label= CDR2 /note= "complementarity determining region

23. .35
/label= CDR1
/note= "complementarity determining region 1"

Location/Qualifiers

This polypeptide sequence comprises the light chain variable region (VL) of human carcinoembryonic antigen (hCEA)-specific antibodies CEA1, CEA2, and CEA3. WH (AAAT7212-313) and VL (AAAT7213-35) gene sequences were obtained for anti-hCEA antibodies CEA1-CEA7 (see AAM19876-85). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 -8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-83 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include yairings of VH and VL sequences from CEA1-7, or their CDS sequences, as well as CEA6 VH and VL variants. (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for disgnosing cancer, e.g. adenocarcinoma of the colon, lung or breast Sequence 111 AA;

Specific binding members for human carcinoembryonic antigen - bind t A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing cancer.

Claim 14; Fig 1b; 128pp; English.

Mccafferty JG;

WPI; 1997-319779/29.

Query Match
100.0%; Score 35; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels

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AAU02542 standard; protein; 111 AA. AAU02542 ID AAU0 XX AC AAU0

RESULT 10

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CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

dwards BM, Main SH, WPI; 2001-282031/29.

N-PSDB; AAS03451

11-OCT-2000; 2000WO-GB003900

12-OCT-1999;

WO200127279-A1. Homo sapiens.

19-APR-2001

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Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                   Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
                    Anti-adipocyte monoclonal antibody light chain, FAT 30.
                                                                                                                                    (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                       Claim 1; Page 118-119; 182pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU02551 standard; protein; 111 AA
                                                                                                                                                    Vaughan TJ;
                                                                                                                      99US-0158812P
                                                                                                       11-OCT-2000; 2000WO-GB003900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
       29-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                    2001-282031/29
                                                                                                                                                                                                                                                                                                                                                                                                                         DVSKRPS 7
                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                            N-PSDB; AAS03442
                                                                                                                                                                                                                                                                                                                                                                             Sequence 111 AA;
                                                                          WO200127279-A1.
                                                                                                                        12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-AUG-2001
                                                            Homo sapiens.
                                                                                                                                                     Edwards BM,
                                                                                         19-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU02551;
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                                                                                                                                                                                                          diseases
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ANU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
chesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
cy complement mediated lysis. The antibodies may be labeled with a
detectable label such as radiolabel, fluorescent or chemical group and
cy used in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
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Gaps ; 100.0%; Score 35; DB 4; Length 111; 100.0%; Pred. No. 6.1; cive 0; Mismatches 0; Indels

Anti-adipocyte monoclonal antibody light chain, FAT 37.

Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.

AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid

sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,

and heavy chain complementarity determining regions (CDR) of the

invention. The antibodies can be used in the treatment of obesity and

cobesity related diseases. The antibodies can be used to deliver drugs or

cobesity related diseases. The antibodies binding specifically to

can be used as a therapeutic itself. Antibodies binding specifically to

adipocytes can be used to activate the immune system to destroy the cells

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cy treather habel such as radiolabel, fluorescent or chemical group and

cy used in methods of diagnosis in human subjects e.g. to determine the

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cy the antibodies can be used as an alternative means of treatment for obese

cy the introduce of adipocyte of fat deposits can also be produced e.g. intra
cy for different types of fat deposits can also be produced e.g. intra
abdominal fat associated with heart disease ö Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related Gaps ö 100.0%; Score 35; DB 4; Length 111; 100.0%; Pred. No. 6.1; 0; Indels 0; Mismatches Claim 1; Page 124; 182pp; English. Query Match
Best Local Similarity 100. DVSKRPS 58 1 DVSKRPS 7 Sequence 111 AA, diseases ઠે ద

Anti-adipocyte monoclonal antibody light chain, FAT 72. (first entry) 29-AUG-2001 AAU02585;

AAU02585 standard; protein; 111 AA.

AAU02585

fat; Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.

WO200127279-A1

19-APR-2001

11-OCT-2000; 2000WO-GB003900.

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C007 77:65:01 C
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(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY. BM, Main SH, Vaughan TJ; 99US-0158812P. 12-OCT-1999; Edwards

WPI; 2001-282031, N-PSDB; AAS03485

2001-282031/29

Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases.

Claim 1; Page 146; 182pp; English.

AAU02501-AAU02535, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of boseity and
cobesity related diseases. The antibodies can be used to deliver drugs or
cobesity related diseases. The antibodies binding specifically to
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
complement mediated lysis. The antibodies may be labeled with a
complement mediated lysis in human subjects e.g. to determine the
constant of adipocyte antigon on the surface of an adipocyte to detect or
confidence of adipocyte antigon on the surface of an adipocyte to detect or
confidence confidence of adipocytes and adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
confidence than undergoing surgery to remove excess fat. Antibodies
confidence types of fat deposits can also be produced e.g. intraconfidence of adipocyte with heart disease

Sequence 111 AA;

Gaps ö 100.0%; Score 35; DB 4; Length 111; 100.0%; Pred. No. 6.1; Live 0; Mismatches 0; Indels Query Match
Best Local Similarity 100...

57 DVSKRPS 7 DVSKRPS -21

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ADK17416 standard; protein; 111 AA. ADK17416;

06-MAY-2004 (first entry)

Anti-human CXCR4 loop 6 ScFv antibody Vl region.

anti-HIV; cytogtatic; virucide; single chain antibody; antibody; yeast; HIV; cancer; CCR5.

Synthetic.

WO2003066830-A2.

14-AUG-2003

07-FEB-2003; 2003WO-US003763

08-FEB-2002; 2002US-00071866. 08-FEB-2002; 2002US-00072031. 25-APR-2002; 2002US-00133978.

(GENE-) GENETASTIX CORP

ï Pauling MH, Zhu Hua S,

WPI; 2003-731501/69

Selecting an acFv against a peptide target by expressing a target fusion protein having a DNA binding domain or activation domain of a transcription activator, useful for diagnosing, preventing and/or treating HIV infection and cancer.

Claim 123; SEQ ID NO 61; 150pp; English

The invention relates to a method of selecting a single chain antibody (scFv) against a peptide target in a yeast by expressing a library of scr fatalon proteins in yeast cells, expressing a target fusion protein in the yeast cells expressing the scFv fusion proteins having either the in the yeast cells expressing the scFv fusion proteins having either the DNA binding domain or the activation domain of the transcription cc activator which is not comprised in the scFv fusion proteins, and a target peptide, and selecting those yeast cells in which a reporter gene is expressed. Each scFv fusion protein comprises either an activation domain or a DNA binding domain of a transcription activator and a scFv having a heavy chain of a variable region (WH) of antibody whose sequence variable region (WL) of antibody whose sequence varies within the library, a light chain of a variable region (VL) of antibody whose sequence varies within the library independently of the Cr antibody whose sequence varies within the library independently of the creporter gene is activated by a reconstituted transcriptional activator formed by binding of the scFv fusion protein to the target fusion for an enthods and compositions of the present invention are useful for preventing and/or treating HIV infection and cancer. This sequence corresponds to the VI region of an anti-human CXCR4 loop 6 antibody gene and used to generate the scFv antibody of the invention.

Sequence 111 AA;

Gapв 100.0%; Score 35; DB 7; Length 111; 100.0%; Pred. No. 6.1; cive 0; Mismatches 0; Indels Ouery Match Best Local Similarity 100... 7; Conservative

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RESULT 14

ADG42838 standard; protein; 111 AA.

ADG42838;

scFv Ab124 light chain variable region.

07-FEB-2003; 2003US-00360828

(HUAS/) HUA S. (PAUL/) PAULING M H. (ZHUL/) ZHU L.

Zhu L; Pauling MH, Hua S,

ô 0; Indels

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ADG42838

(first entry) 26-FEB-2004 HIV infection; HIV type 1; HIV type 2; cancer; breast, prostate; liver; renal; lung; skin; ovarian; cervical; brain; thyroid; stomach; colon; lymphoma; leukaemia; pancreas; chemokine receptor; antibody.

Synthetic.

JS2003206909-A1.

06-NOV-2003.

08-FEB-2002; 2002US-00071866. 08-FEB-2002; 2002US-00072301. 25-APR-2002; 2002US-00133978.

WPI; 2004-051479/05

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP,
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Ru Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietze
Patury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human diagnostic and therapeutic pprotein SEQ ID NO:5321
                                                                                                                                                                                                                                                                                                                                                                                  ABM85072 standard; protein; 214 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; Page; 190pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-SEP-2002; 2002US-0410259P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-2003; 2003WO-US028227.
                                                                                                                                                                                                                                                                                                                                                                                                                                        18-NOV-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                   DVSKRPS 58
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N-PSDB; ADG42836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in gene mapping.
                                                                                                                                                                                                               Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004023973-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                              ABM85072;
                                                                                                                                                                                                                                                                                                                                                           RESULT 15
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Gietzen D;

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The invention relates to an antibody that binds to loop 6 of human chemokine receptor (CXCR4). The antibody is useful in the treatment or prevention of HIV infection (e.g. HIV type 1 and HIV type 2) and cancer of (e.g. breast, prostete, liver, renal, lung, skin, ovarian, cervical, brain, thyroid, stomach, colon, lymphoma, leuksemia and pancreas cancer cells), for screening drugs, for diagnosing disease or condition associated with interaction with chemokine receptor. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Antibody binding loop of human chemokine receptor useful for the treatment of HIV infection and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 35; DB 8; Length 111; 100.0%; Pred. No. 6.1; cive 0; Mismatches 0; Indels
                                                                                                                 Claim 6; SEQ ID NO 61; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
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Best Local Similarity
Matches 7; Conserv
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constitute of the invention may have a use in gene therapy. The human clasmostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorders, gastrointestinal disorders, or disorder, neurological disorders, gastrointestinal disorders, or confecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide from minute biological samples, in detecting single nucleotide gone therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                          8; Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 35; DB
100.0%; Pred. No. 12;
:ive 0; Mismatches
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                     Sequence 214 AA;
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Sequence 53, Appl
Sequence 53, Appl
Sequence 33, Appl
Sequence 53, Appl
Sequence 42, Appl
Sequence 17, Appl
Sequence 53989, A
Sequence 5577, Ap
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15, Appl
19, Appl
19, Appl
19, Appl
25, Appl
12, Appl
12, Appl
10, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, A Sequence 15, A Sequence 19, A Sequence 19, A Sequence 19, A Sequence 25, A Sequence 112, A Sequence 10, A Sequence 11, A Seque
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/ReCOMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-652-B16A-15
US-09-490-10A-19
US-09-490-153-19
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US-09-383-667-25
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US-09-420-153-19
US-09-420-153-19
US-09-420-16-10
US-09-56-098-10
US-09-58-10A-13
US-09-383-916-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      513545 seqs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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35
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
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Sequence 43922, A Sequence 18161, A Sequence 15, App Sequence 11, Appl Sequence 2, App Sequence 15, App Sequence 15, App Sequence 11, Appl Sequence 1796, App Sequence 33297, A Sequence 2476, App Sequence 2416, App Sequence 2411, App Sequence 2416, App Sequence 2411, App Sequence 24311, App Sequence 3333, App Sequence 3333, App Sequence 3333, App	
US-09-270-767-43922 US-09-222-991A-18161 US-08-867-941-15 US-08-867-941-11 US-08-867-941-11 US-09-318-092-423 US-09-318-092-423 US-09-074-658-15 US-09-074-658-15 US-09-107-532A-7296 US-09-107-532A-7296 US-09-276-767-38080 US-09-276-767-38080 US-09-276-767-38080 US-09-276-767-38080 US-09-276-767-38080 US-09-276-767-38080 US-09-276-767-38080 US-09-278-767-53297 US-09-2889-207A-476 US-09-2889-207A-476 US-09-2881-207A-476 US-09-583-110-4891	
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ALIGNMENTS

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REGULT 1

O'S-09-183-667-14

Sequence 14 Application Us/09383667

Sequence 14 Application Us/09383667

Sequence 14 Application Us/09383667

Sequence 15 Application Us/09383667

GENERAL INFORMATION

APPLICANT: Decaux. Brightee

APPLICANT: Decaux. Brightee

APPLICANT: Sugget., Ballib E.

Best Local Similarity 100.04; Score 35; DB 4; Length 7;

Best Local Similarity 100.04; Score 35; DB 4; Length 7;

Best Local Similarity 100.04; Score 35; DB 4; Length 7;

Best Local Similarity 100.04; Score 35; DB 4; Length 7;

Best Local Similarity 100.04; Score 35; DB 4; Length 7;

Best Local Similarity 100.04; Score 35; DB 4; Length 7;

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Best Local Similarity 100.04; Score 35; DB 4; Length 7;

Best Local Similarity 100.04; Score 35; DB 4; Length 7;

Best Local Similarity 100.04; Score 35; DB 4; Length 7;

Best Local Similarity 100.04; Score 35; DB 4; Length 7;

Best Local Similarity 100.04; Score 35; DB 4; Length 7;

Best Local Similarity 100.04; Score 35; DB 4; Length 7;

Best Local Similarity 100.04; Score 35; DB 4; Length 7;

Best Local Similarity 100.04; Score 35; DB 4; Length 7;

Best Local Similarity 100.04; Score 35; DB 4; Length 7;

Best Local Similarity 100.04; Score 35; DB 4; Length 7;

Best Local Simi
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ATTORNEY/AGENT INFORMATION
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 DVSKRPS 58
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New York
New York
Y: USA
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CITY: Ne
STATE: N
COUNTRY:
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Sequence 19, Application US/09025769B

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Re, Liming
APPLICANT: Poleckhum, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 35; DB 2; Length 111; 100.0%; Pred. No. 1.9; tive 0; Mismatches 0; Indels
                              COUNTRY: United States of America COMPUTER: Indicate Pork!

MEDIUM TYPES Floppy disk COMPUTER: IBM PC COMPATED POSS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) SURPAYARE: Patentin Release #1.0, Version #1.25 (EPO) SUPPLICATION NUMBER: US/08/652,816A PRIOR APPLICATION NUMBER: GB 912579.4 FILING DATE: 02-DEC-1991

PRIOR APPLICATION NUMBER: GB 912579.8 FILING DATE: 02-DEC-1991

PRIOR APPLICATION NUMBER: GB 9206318.9 FILING DATE: 24-MAR-1992

PRIOR APPLICATION NUMBER: GB 9206318.9 FILING DATE: 23-SEP-1992

PRIOR APPLICATION NUMBER: GB 9206372.6 FILING DATE: 07-DEC-1995

PRIOR APPLICATION NUMBER: GB 9206372.6 FILING DATE: 07-DEC-1995

PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 9510824.6 FILING DATE: 07-DEC-1995

PRIOR APPLICATION NUMBER: GB 952504.9 FILING DATE: 07-DEC-1995

PRIOR APPLICATION NUMBER: GB 952504.9 FILING DATE: 07-DEC-1995

PRIOR APPLICATION NUMBER: GB 952504.9 FILING DATE: 07-DEC-1995

PRIOR APPLICATION NUMBER: GB 95210240

FILING DATE: 07-DEC-1995

PRIOR APPLICATION NUMBER: US 08/244,597

FILING DATE: 07-DEC-1995

PRIOR APPLICATION NUMBER: US 08/244,597

FILING DATE: 07-DEC-1995

PRIOR APPLICATION NUMBER: US 08/244,597

FILING DATE: DA-1944

ATTORNEY/AGENT INFORMATION: NAME: DA-104 W. Clough REGISTARTION NUMBER: 36.107

RESEISTARTION NUMBER: 36.107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100...
Lag 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DVSKRPS 7
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STATE: D.C.
COUNTRY: USA
TIP: 20006
UTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 35; DB 3; Length 112; 100.0%; Pred. No. 1.9; tive 0; Mismatches 0; Indel8
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ENDRY disk
COMPUTER: Floppy disk
COMPUTER: PACENTIN ELEGAGE #1.0, Version #1.30 (EPO)
SOFTWARE: PACENTIN Release #1.0, Version #1.30 (EPO)
SOFTWARE: PACENTIN DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 19:
SEQUENCE GIRRACTERISTICS:
LENGTH: 112 amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: amino acide
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LING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
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us-10-614-959-14.ra

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STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
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US-09-490-153-19
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CITY: New York
CITY: New York
STATE: New York
COUNTRY: USA
ZIF: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/490, 153
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: US/09/025, 769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
                                                                                                                                                                                                                                                                                                                                       Ouery Match
100.0%; Score 35; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Knappik, Achim
Pack, Peter
Ind, Vic
Ge, Liming
Moroney, Simon
PITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
      REGISTRATION NUMBER: 31,298
REPREBNICE/DOCKET WINDBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                            LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: cUnknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-490-070A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-09-490-153-19
; Sequence 19, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
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52 DVSKRPS 58
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                                                                                                                                                                                                                                                                                                                        APPLICANT: Knappik, Achim
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
Query Match
Best Local Similarity 100.0%; Score 35; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels
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100.0%; Score 35; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indele
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FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: protein SEQ ID NO: 19: US-09-490-324-19
                                                                                                                                                                                                                                                           Sequence 19, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
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US-09-383-667-25
; Sequence 25, Application US/09383667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 19
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Sequence 125, Application US/09424840B

Patent No. 6790338

GENERAL INFORMATION:

APPLICANT: Berchtchid, Peter

APPLICANT: Berchtchid, Peter

TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES

FILE REFERENCE: 100564-09049

CURRENT APPLICATION NUMBER: US/09/424,840B

CURRENT FILING DATE: 1999-12-03

PRIOR FILING DATE: 1998-05-08

PRIOR FILING DATE: 1998-05-08

PRIOR FILING DATE: 1997-12-12

PRIOR FILING DATE: 1997-12-12

PRIOR FILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 128

SOFTHAME: PATENTING DATE: 1997-06-06
Patent No. 6624295
GENERAL INFORMATION:
APPLICANT: Adams, Camelia W.
APPLICANT: Baton, Dan B.
APPLICANT: Baton, Dan B.
APPLICANT: Baton, Dan B.
APPLICANT: Wide, J. Kevin
APPLICANT: Wide, J. Kevin
APPLICANT: Suggett, Shelley
TITLE OF INVENTION: Human Anti-Factor IX/IXA Antibodies
FILE REFERENCE: P1661R2
CURRENT APPLICATION NUMBER: US 60/9933, 667
CURRENT FILING DATE: 1999-08-26
EARLIER PILING DATE: 1999-08-26
EARLIER FILING DATE: 1999-08-28
EARLIER FILING DATE: 1999-03-03
NUMBER: US 60/122,767
NUMBER OF SEQ ID NOS: 32
LENGTH: 7
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88.6%; Score 31; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 0; Indels
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4.1e+05;
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85.7%; Pred. No. 4.1e+05
:ive 1; Mismatches
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US-08-378-939-12
Sequence 12, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
APPLICANT: CROWE, JAMES SCOTT

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Best Local Similarity 85.7
Matches 6; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 10. Application US/08487550

Fatent No. 6113898

GENERAL INFORMATION:
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF,
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 PAINCE Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
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APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFRATING SYSTEM: PC-DOS/MS-DOS
SOFRATING SYSTEM: PC-DOS/MS-DOS
SOFRWATING SYSTEM: PC-DOS/MS-DOS
SOFRWATING SYSTEM: PC-DOS/MS-DOS
SOFRWATING SYSTEM: VE-DOS/MS-DOS
SOFRWATING SYSTEM: VE-DOS/MS-DOS
SOFTWARE: PATENTICATION DATA:
APPLICATION NUMBER: US/08/378,939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.6%; Score 31; DB 2;
85.7%; Pred. No. 33;
iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION 1935

PRIOR APPLICATION NUMBER: US 07/952640

FILING DATE: 01-DEC-1992

ATTORNEY/AGENI INFORMATION:

NAME: ERNST, BARBARA G

REGISTRATION NUMBER: 1808-118

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 1880-6040

TELEPHONE: (202) 783-6040

TELEPHONE: (202) 783-6031

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.6
Best Local Similarity 85.7
Matches 6; Conservative
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2; Mismatches

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us-10-614-959-14.rai
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ATTORNEY/AGENT INFORMATION:

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5; Conservative
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LENGTH: 236 amino acids
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                                                                                                                               71 DINKRPS 77
                                                                                  1 DVSKRPS 7
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71 DINKRPS 77
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US-09-949-016-7859
   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "O HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: 12
CORRESPONDENCE ADDRESS: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.6%; Score 31; DB 3; Length 236; 71.4%; Pred. No. 33;
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Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
NAME: TEBKIN, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE DOCKET NUMBER: 012712-131
TELECOMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: 09/487,550
FILING DATE: 07-JUM-1995
ATTONNEY,AGENT INFORMATION:
NAME: TESKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE,DOCKET NUMBER: 35,030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-09-526-098-10
Sequence 10, Application US/09526098
Patent No. 6492134
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 236 amino acids
TYPE: amino acid
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Best Local Similarity 71.4
Matches 5; Conservative
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; MOLECULE TYPE: protein
US-08-487-550-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-09-526-098-10
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71 DINKRPS 77
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Best Local Similarity
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US-09-369-364A-13

Sequence 13, Application US/09369364A

Patent No. 6391610

GENERAL INFORMATION:

APPLICANT: Hurekainen, Tiina L.

SACONERI SALONON: 324007/10-30-00

CURRENT FILING DATE: 1999-08-06

NUMBER OF SEQ ID NOS: 31

SEQ ID NO 13

LENGTH: 1882

TYPE: PRT

ORGANISM: HOMO Sapiens ADAMTS-9

FEATURE:

NAME/KEY: MOD RES

LOCATION: (451)

OTHER INFORMATION: Xaa = C

NAME/KEY: MOD RES

LOCATION: (521)

OTHER TANDALIZANI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 33, Application US/09025769B
; Sequence 33, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
APPLICANT: Rack, Peter
APPLICANT: Pack, Peter
APPLICANT: Ge, Liming
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.6%; Score 31; DB 3; Lt
100.0%; Pred. No. 3.1e+02;
tive 0; Mismatches 0;
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Xaa = Y
US-09-369-364A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 6, Conservative
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          1 DVSKRP 6
                                                                                                                                                                                               , TYPE: PRT
, ORGANISM: Human
US-09-949-016-7859
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US-09-025-7698-33
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STREET: 1251 Avenue of the Americas
COMPUTER: New York
STATE: New York
STATE: New York
STATE: New York
The 10021
COMPUTER READALE FORM:
COMPUTER: LIBM PC Compatible
COMPATION NUMBER: LIBM PC COMPATION
COMPATIBLE
COMPATION NUMBER: LIBM COMPATION
COMPATION FOR SEQ IN NO: 33:
COM
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us-10-614-959-14.rapk
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October 14, 2005, 16:20:10 ; Search time 49.7656 Seconds (without alignments) 58.615 Million cell updates/sec
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(SGNZ_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

(SGNZ_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

(SGNZ_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

(SGNZ_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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(SGNZ_6/ptodata/2/pubpaa/US16_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1859788
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1859788 seqs, 416717961 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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35
1 DVSKRPS 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Description	Special Specia	Sequence on annual sequence	ζ.		5	ia	000	Semience 2065	Semience 2055, Ap	Semionce 24 Anni	Sequence 40. Appl
		ID	US-10-308-817-98	US-10-453-698-98	US-10-447-331-1	US-10-360-828-61	US-10-916-758-42	US-09-880-748-1898	US-10-293-418-1898	US-09-880-748-2055	US-10-293-418-2055	US-10-981-692-24	US-10-981-692-40
		В			15						15		
	Query	Length	66	66	110	111	118	240	240	241	241	242	242
*	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
		Score	35	35	35	35	35	35	35	35	35	35	35
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Seguence 1927. Ap	192	29.	equence 33.	equence 26.	equence 192	192	324	Sequence 31, Appl	36.	191	191	191	91	144	68	68	70	89	92	equence 1934	144	1682	168	Sequence 1707, Ap	1899	1926	1934	46.	77.	quence 88,	91,	96	m
09-880-748-192	10-293-418-1	10-981-692-2	10-981-692-3	10-981-692-	09-880-748-192	10-293-418-1	10-293-418-324	10-981-69	10-981-692-3	19-880-748-1	-880-748-19	10-293-418-19	10-293-418-19	19-880-748-1	9-880-748-16	19-880-748-16	19-880-748-17	9-880-748-18	19-880-748-	9-880-748-1	.0 - 293 - 418 - 1	.0 - 293 - 418 - 168	.0-293-418-16	.0-293-418-170	0-293-418-18	.0-293-418-192	0 - 293 - 418 - 193	-10-935-290-4	-10-935-290-7	-10-935-290-8	-935-290	-10-935-290-9	-10-935-290-1
10	12	18	18	18	10	15	15	18	18	10	10	15	15	10	10	10	10	10	10	2	15	15	15	12	15	12	15	11	11	11	17	11	11
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100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	8	100.0	00	100.0	8	100.0	ë.	8	100.0	ė.	ö	ė.	100.0	8	8	100.0	9	100.0
35	35	ij	32	32	35	32	32	32	32	35	35	35	32	32	32	32	32	35	32	32	32	32	35	32	32	32	9	32	35	32	32	32	32
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	78	53	30	31	32	33	34	35	36	37	80 1	39	40	41	42	43	44	45

ALIGNMENTS

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Gaps
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Best Local Similarity 100.0%; Pred. No. 15; Length 99; Matches 7; Conservative 0; Mismatches 0; Indels
          Squence 98, Application US/10308817
Fublication No. US20030219861A1
GENERAL INFORMATION:
APPLICANT: Nother, Russell
APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin version 3.1
SEQ ID NO 98
LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 98, Application US/10453698; Publication No. US20040038308A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 DVSKRPS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DVSKRPS 7
                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: human
US-10-308-817-98
US-10-308-817-98
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US-10-453-698-98
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US-09-880-748-1898
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publication No. US2003020690A1

general information:

general information:

APPLICANT: Hua, Shaobing

APPLICANT: Zhu, Li

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS

CURRENT APPLICATION NUMBER: US/10/360,828

CURRENT FILING DATE: 2003-02-07

PRIOR FILING DATE: 2002-02-08

PRIOR FILING DATE: 2002-02-08

PRIOR APPLICATION NUMBER: US 10/072,301

PRIOR APPLICATION NUMBER: US 10/072,301

PRIOR APPLICATION NUMBER: US 10/13,978

PRIOR APPLICATION NUMBER: US 10/133,978

HUMBER OF SEQ ID NOS: 64
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Pred. No. 15;
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; Sequence 1. Application US/10447331
; Eublication No. US2003029434A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Carter, Paul J.
; APPLICANT: Carter, Paul J.
; TITLE OF INVENTION: ANTIBODIES FOR CANCER THERAPY AND TITLE OF INVENTION: DIRACOSIS
; TITLE OF INVENTION: DIRACOSIS
; FILE REFERENCE: GENENT.122A
; CURRENT APPLICATION NUMBER: US/09/515,825
; PRIOR APPLICATION NUMBER: US/09/515,825
; PRIOR FILING DATE: 1999-03-01
; PRIOR PLING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTERO FOR WINGOWS Version 4.0
; SEROID NO. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                         0; Mismatches
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 82 CIP (1087-37 CIP)
CURRENT APPLICATION NUMBER: US/10/453,698
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Patentin version 3.2
LENGTH: 99
                                                                                                                                                                                                                                                                               100.0%;
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Best Local Similarity 100.
Matches 7; Conservative
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Matches 7; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 DVSKRPS 58
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                                                                                                                                                                                                                                                                                                                                                                       1 DVSKRPS 7
                                                                                                                                                                                      TYPE: PRT
CRGANISM: human
US-10-453-698-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-360-828-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                               Query Match
100.0%; Score 35; DB 15; Length 111;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Synthetically generated peptide US-10-916-758-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 35; DB 18;
100.0%; Pred. No. 18;
iive 0; Mismatches 0;
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; Sequence 42, Application US/10916758
; Publication No. US20050180977A1
; GENERAL INFORMATION:
; APPLICANT: Madison, Edwin L.
; TITLE OF INVENTION: ENDOTHELIASE-2 LIGANDS
; FILE REFERENCE: 10280-065001
; CURRENT APPLICATION NUMBER: US/10/916,758
; CURRENT APPLICATION NUMBER: US/10/916,758
; CURRENT FILING DATE: 2004-08-12
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
                                                                                        CTHER INFORMATION: VL Of BCFV Ab124 US-10-360-828-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
SOFTWARE: Patentin version 3.1 SEQ ID NO 61 LENGTH: 111
                                               TYPE: PRT ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1898
LENGTH: 240
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CRGANISM: Homo sapiens US-09-880-748-1898

ö Query Match
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels (181 DVSKRPS 187 셤 ò

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Gaps

RESULT 7

US-10-293-418-1898

Sequence 1898 Application US/10293418

Publication No. US2003022396A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

CURRENT FILION Antibodies that Immunospecifically Bind BLyS

CURRENT FILION NUMBER: US/10/293,418

PRIOR PPLICATION NUMBER: 00/331,469

PRIOR PILING DATE: 2001-11-16

PRIOR PILING DATE: 2001-12-19

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-25

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247

SEQ ID NO 1898

LENGTH: 240 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-293-418-1898

ö 100.0%; Score 35; DB 15; Length 240; 100.0%; Pred. No. 36; tive 0; Mismatches 0; Indels Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative

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RESULT 8 US-09-880-748-2055

Sequence 2055, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPRENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR PPLING DATE: 2000-10-15
PRIOR PPLING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILING DATE: 2000-10-17

Query Match
100.0%; Score 35; DB 10; Length 241;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0 /
SEQ ID NO 2055 TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-2055

182 DVSKRPS 188 1 DVSKRPS 7 g

Gaps

US-10-293-418-2055

US-10-293-418-2055

Sequence 2055, Application US/10293418

Sequence 2055, Application US/10293418

Sequence 2055, Application US/10293418

SEQUENCE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

TILE REPERBNCE: PF523P2

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR PILING DATE: 2001-11-16

PRIOR PILING DATE: 2001-12-19

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2000-103-16

PRIOR PILING DATE: 2000-103-16

PRIOR FILING DATE: 2000-10-17

PR ; TYPE: PRT ; ORGANISM: Homo US-10-293-418-2055 Query Match

100.0%; Score 35; DB 15; Length 241;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels Indela

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US-10-981-692-24

Sequence 24, Application US/10981692

Publication No. US20050163777A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B

FILE REFERENCE: PF590P1

CURRENT APPLICATION NUMBER: US/10/981,692

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RESULT 14
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; Sequence 40, Application No. US20050163777A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR FILING DATE: 2004-11-05
; PRIOR FILING DATE: 2003-05-29
; PRIOR FILING DATE: 2003-05-29
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
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Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFRENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16
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Pred. No. 37;
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CURRENT FILING DATE: 2004-11-05
PRIOR APPLICATION WUMBER: PCT/US03/16802
PRIOR FILING DATE: 2003-05-29
PRIOR FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 76
SOFWARE: PATENTIN VERSION 3.1
SEQ ID NO 24
LENGTH: 242
TYPE: PRT
ORGANISM: Artificial sequence
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US-10-981-692-40
                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: NO15E08 scFv
US-10-981-692-24
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Best Local Similarity 100.0%;
Matches 7; Conservative 0
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Sequence 29, Application US/10981692
Publication No. US20050163777A1
SEPERATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
FILE REPERENCE PES90P1
CURRENT APPLICATION UNMER: US/10/981,692
CURRENT FILING DATE: 2004-11-05
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Sequence 1927, Application US/10293418

Publication No. US20030223996A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: RUben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2001-11-27

PRIOR FILING DATE: 2001-11-6

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-6-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-17

PRIOR PRIOR FILING DATE: 2001-01-17

PRIOR PRIOR PRIOR DATE: 2001-01-17
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100.0%; Score 35; DB 15; Length 243;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 35; DB 10; Length 243; 100.0%; Pred. No. 37; tive 0; Mismatches 0; Indels 0
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SEQ ID NO 1927
LENGTH: 243
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Best Local Similarity 100.
Matches 7; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-880-748-1927
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Page 5
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PRIOR APPLICATION NUMBER: PCT/US03/16802
PRIOR FILING DATE: 2003-05-29
PRIOR APPLICATION WUMBER: 60/383,802
PRIOR FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 76
SEQ ID NOS: 76
SEQ ID NO 29 entIn version 3:1
LENGTH: 243
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
COTHER INFORMATION: N024E07 scFv
US-10-981-692-29
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Query Match 100.0%; Score 35; DB 18; Length 243; Best Local Similarity 100.0%; Pred. No. 37; Matches 7; Conservative 0; Mismatches 0; Indels (183 DVSKRPS 189 1 DVSKRPS 7 g

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Gaps

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TYPE: PRT ORGANISM: Artificial sequence

FEATURE: GOTHER INFORMATION: N023E01 SCFV US-10-981-692-33

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Best Local Similarity 100.0%; Pred. No. 37;

Matches 7; Conservative 0; Mismatches 0; Indels (

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183 DVSKRPS 189 셤

Search completed: October 14, 2005, 17:00:44 Job time : 50.7656 secs

us-10-614-959-14.rapk

1 DVSKRPS 7 ઠે

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OM protein - protein search, using sw model

October 14, 2005, 16:02:59 ; Search time 9.73438 Seconds (without alignments) 69.190 Million cell updates/sec Run on:

US-10-614-959-14 35 1 DVSKRPS 7 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

0

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Ig lambda chain - 60s ribosomal prot hypothetical prote hypothetical prote	hypothetical prote mutants block spor thloredoxin-disulf	Liloredoxin reduct thioredoxin reduct familial Alzheimer SRPM54 procein - M hypothetical prote hypothetical prote	gene 12 protein - 4-hydroxybutyryl-C pseudolysin (EC 3.
S14675 T40075 A64624 D71891 A82017	AE0243 E83999 B97777	G87604 S65358 S35481 T40769	22BPC2 F90422 HYBSPA
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23 25 29 300	301 309 310	344 444 6440 723	4 5 8 4 6 3 8 9 8
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ALIGNMENTS

Сарв ö Query Match

100.0%; Score 35; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels

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Cispecies: Arabidopsis thaliana (mouse-ear cress)
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Gaps ö Query Match 97.1%; Score 34; DB 2; Length 646; Best Local Similarity 85.7%; Pred. No. 12; Matches 6; Conservative 1; Mismatches 0; Indels

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antibody light chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Accession: 551149
R;de Kruif, J; Boel, E.; Logtenberg, T.
Submitted to the EMBL Data Library, January 1995
R;de Kruif, J; Boel, E.; Logtenberg, T.
A;Description: Selection and application of human SCFV antibody fragments from a semi-syr
A;Reference number: 551147
A;Recession: 551149
A;Residues: preliminary
A;Residues: 1.110 CDEK>
A;Accession: 1.110 CDEK>
A;A
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typecies: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: F64690
C;Accession: F64690
C;Accession: F64690
A;Reiley, J.M.; Cotton, M.D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne)
Peterson, S; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne)
Ron, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.A.
A;Aitle: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reserence number: A64520; MulD:97394467; PMID:9252185
A;Accession: F64690
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-423 «TOM»
A;Residues: 1-423 «TOM»
A;Cross-references: UNIPROT:025919; GB:AE000637; GB:AE000511; NID:g2314536; PIDN:AAD0841(
         A;Cross-references: GDB:119342; OWIM:147240
A;Cross-references: GDB:119342; OWIM:147240
A;Rap position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp C;Complex: An immunoglobulin heterotetramer subunits associate into landa disulfide bonds. In some cases, such as ISA and IGM, the subunits associate into landa cisuperfamily: immunoglobulin v region; immunoglobulin homology
C;Reywords: blocked amino end; heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology < IMM>
F;16-92/Domain: immunoglobulin homology < IMM>
F;16-99/Disulfide site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status F;22-90/Disulfide bonds: #status predicted
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A;Cross-references: EMBL:X83712
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;13-90/Domain: immunoglobulin homology <IMM>
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Pred. No. 9.8;
1; Mismatches
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Pred. No. 23;
1; Mismatches
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Pred. No. 5.9;
1; Mismatches
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Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.4%;
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Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.71
Matches 6; Conservative
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A; Gene: GDB: IGLV@
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R; Editiz, M.; Linke, R.P.
Biochem. Biophys. Res. Commun. 194, 1427-1434, 1993
A; Title: The precursor molecule of a V-lambda II-immunoglobulin light chain-derived amyla. Reference number: A38923; MUID:93356823; PMID:8352801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig lambda chain V-II region (Tro) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: John 1981 #sequence_revision 29-Jul-1981 #text_change 09-Jul-2004
C;Accession: A01973
R;Scholz, R; Yang, C.; Hilschmann, N.
R;
                                                                                                                                                                                                                                      Ig lambda chain V-II region (Har) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 16-Aug-1996
C;Accession: A24626
R;Eulitz, M.; Linke, R.
Biol. Chem. Hoppe-Seyler 366, 907-915, 1985
A;Title: Amyloid fibrils derived from V-region together with C-region fragments from a A;Reference number: A24626; MUID:86077295; PMID:3935132
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AjAccession: A38923
AjAccession: A38923
AjAccession: A38923
AjAccession: A38923
AjAccession: A38923
AjAccession: Association
Ajaccession: Association
Cjacciation: 195;96-103
Cjacciation: This protein is derived from an immunoglobulin light chain of lambda type.
Cjacciation: This protein is derived from an immunoglobulin homology
Cjacciation: Immunoglobulin V region; immunoglobulin protein #status predicted <WAT>
F;7-83/Domain: immunoglobulin homology <IMM>
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C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
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A;Residues: 1-60 <EUL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 103
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A;Residues: 1-111 <SCH>
A;Cross-references: UNIPROT:P01707
C;Commert: This chain was isolated from a myeloma protein.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.4%; Score 32; DB 2;
85.7%; Pred. No. 5.4;
rative 1; Mismatches
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Pred. No. 3.1;
1; Mismatches
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                              612
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|DVNKRPS 49
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DISKRPS
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A38923

Matches

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submitted to the EMBL Data Library, January 1993
A;Description: V-lambda-2 gene sequence of a high affinity anti-idiotypic IgM antibody f!
A;Reference number: S31515
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C. Species: Hono sapiens (man)
C. Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C. Species: Hono sapiens (man)
C. Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C. Accession: S44105
A. Standarina, R. B.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
A. Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable re
A. Rescription: Idiotypic vaccination against human B-cell lymphoma: rescue of variable re
A. Recession: S44105
A. Recession: S44105
A. Residues: 1-112 < AAM>
A. Residues: 1-112 < AAM>
A. Residues: 1-112 < AAM>
A. Residues: Inmunoglobulin v region; immunoglobulin homology
C. Superfamily: immunoglobulin homology < IMM>
F:15-92/Domain: immunoglobulin homology < IMM>
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A;Cross-references: UNIPROT:P23191; EMBL:X56977; NID:g44180; PIDN:CAA40298.1; PID:g44182
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Type II site-specific deoxyribonuclease (EC 3.1.21.4) MboII - Moraxella bovis C;Species: Moraxella bovis C;Accession: S26836
R;Bocklage, H.; Heeger, K.; Mueller-Hill, B. Nucleic Acids Res 19, 100-1013, 1991
A;Reference number: S26835; MUID:912177; PMID:2020540
A;Reference number: S26835; MUID:91212177; PMID:2020540
A;Status: preliminary
A;Molecule type: DNA
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83.3%; Pred. No. 64;
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85.7%; Pred. No. 17;
ive 0; Mismatches
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Pred. No. 17;
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1; Mismatches
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Ig lambda chain V-J region - human
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Best Local Similarity 85.73
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 DVSNRPS 58
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A;Gross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2
C;Complex: An immunoglobulin hererotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin hererotetramer
F;15-22/Domain: immunoglobulin homology <IMM>
F;15-22/Domain: immunoglobulin homology <IMM>
F;17-90/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cjaccession: S36281
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. RshBo J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MUID:93178448; PMID:7679990
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                                                                         Ig lambda chain V-II region (Win) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 09-Jul-2004
C;Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 09-Jul-2004
C;Accession: A01978
R;Chen, B.L.; Chiu, Y.Y.H.; Humphrey, R.L.; Poljak, R.J.
Biochim. Blophys. Acta 537, 9-21, 1978
A;Ttle: Amino acid sequence of the human myeloma lambda chain Win.
A;Reference number: A01978; MUID:79062503; PMID:102365
A;Residues: 1-111 <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S31515
R;van der Heijden, R.W.J.; Uytdehaag, F.G.C.M.; Osterhaus, A.D.M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:218823; NID:g33414; PIDN:CAA79275.1; PID:g939907 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-92/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: S36281
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
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Pred. No. 9.9;
1; Mismatches
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C,Comment: This is a Bence Jones protein.
C,Genetics:
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Best Local Similarity 85.7%;
Matches 6; Conservative
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EVSKRPS 58
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141 NISKRPS 147
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C;Species: Borrella burgdorferi (Lyme disease spirochete)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: E70191
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Pujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Pypothetical protein Atu0540 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C; Species: Agrobacterium tumefaciens C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004 C; Accession: AH2642 C; Accession: AH2642 C; Accession: AH2642 A; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I F; Wood, D.W.; Setubal, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A; Ahathors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Apartors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Apartors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Apartors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Apartors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Apartors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Apartors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, W.; Krespan, W.; Perry, M.; Gordon-Kamm, Apartors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, W.; Krespan, W.; Perry, M.; Gordon-Kamm, Apartors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, W.; Krespan, W.; Perry, M.; Gordon-Kamm, Apartors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, W.; Krespan, W.; Perry, M.; Gordon-Kamm, Apartors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, W.; Krespan, W.; Perry, W.; Gordon-Kamm, Apartors: You, M.; You, M.; You, You, Y.; Biddle, Y.; Yang, Yan
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C;Species: 30-Sep_2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: A59425
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2329, 2001
A;Title: Genome Sequence of the plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: UNIPROT:Q8UHW8; GB:AE007869; PIDN:AAK86354.1; PID:g15155478; GSPDB:q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:QBUHW8; GB:AE008688; PIDN:AAL41558.1; PID:g17738891; GSPDB:d
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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82.9%; Score 29; DB 2; Length 88;
Best Local Similarity 71.4%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 29; DB 2; Length 74;
Pred. No. 19;
1; Mismatches 1; Indels
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Best Local Similarity 71.4%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-74 <KUR>
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Nature 390, S80-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: T70191
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: A137 **CKLE>
A;Residues: J-337 **CKLE>
A;Residues: J-337 **CKLE>
A;Accessinences: UNIPROT:051676; GB:AE001173; GB:AE000783; NID:g2688665; PIDN:AAC67081
A;Experimental source: strain B31
C;Superfamily: translation factor, SUAS type
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Gapa ; Query Match 82.9%; Score 29; DB 1; Length 337; Best Local Similarity 71.4%; Pred. No. 88; Astches 5; Conservative 2; Mismatches 0; Indels

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Search completed: October 14, 2005, 16:23:40 Job time : 11.7344 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

October 14, 2005, 15:51:44; Search time 46.5938 Seconds (without alignments) 76.932 Million cell updates/sec Run on:

US-10-614-959-14 35 1 DVSKRPS 7 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		Description	O9xec7 arabidonala	_	homo	helic					_	-						_			homod	buchn		070918 prunus necr		homo 85	-	078098 neurospora				0 mus	_
SUMMARIES		ID		LV2D HUMAN	Q6P1 <u>Q</u> 7	025919	LV2I HUMAN	Q7MUS6	Q7S4H3	612SL9	Q64WES	Q828G3	Q7SF90	06SLD6	Q75E06	ATS9 HUMAN	BFR1 MAGMG	Q9V6 <u>F</u> 8	Q6PJA3	Q6P5S3	Q9BTM2	Y170 BUCBP	070914	070918	071142	Q86V04	Q9XY82	075098	Q6DHX1	T2M2_MORBO	Q80U48	OSPHC0	Q8CAA2
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æ	Query	Match	97.1	91.4	91.4	91.4	98.6	98.6	88.6	88.6	98.6	98.6	98.6	98.6	88.6	88.6	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	'n	85.7	85.7	85.7	85.7
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O9dbj2 mus musculu O14523 homo sapien O80x80 mus musculu O6d017 erwinia car Q6adp4 leifsonia x Q6lwq4 methanococc O64qq1 bacteroides Q8ax99 drosophila Q9vn46 drosophila Q9vn46 drosophila Q6vey3 vitis vinif Q8uwba agrobacceri Q6lkO5 photobacceri Q7d190 agrobacteri Q6d0t2 erwinia car
Q9DBJ2 TM24 HUMAN TM24 HUMAN TM24 MOUSE Q6DDT Q6ADP4 Q6LWQ4 Q6LWQ1 Q8XS99 Q9VN46 Q6YEY3 Q6TEXQ5 Q7D190
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ALIGNMENTS

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Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

REDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Selberg B., Buetow K.H., Schaefer C.F., Schuler G.D.,

Altechnis R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altechnis R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

An interpreted M.J., Boarle M.S., Carning G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshyuki S., Carninci P., Prange C.,

Brownstein M.J., Workerman K.J., Malber J.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Roshinguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.;

Mannan and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-Lung;
Straubberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC030983; AAH30983.1; -.
HSSP; P01709; 1A8J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 85.7 tes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||:||||
71 DVNKRPS 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DVSKRPS 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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A Scholz R., Yang C., Hilschmann N.;

Thus antibody structure. Primary structure of a human monoclonal

I gal-immunoglobulin (myeloma protein Tro). VI. Amino acid sequence of

The L-chain, lambda-type, subgroup II.";

Hoppe-Scyler's Z. Physiol. Chem. 386:1903-1918(1979).

L. Pope-Scyler's Z. Physiol. Chem. 386:1903-1918(1979).

I MSCELLANEOUS: This chain was isolated from a myeloma protein.

- I - MISCELLANEOUS: This chain was isolated from a myeloma protein.

PRI, A01973; LZHUTR.

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Q6-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                     Score 34; DB 2; Length 646;
Pred. No. 69;
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Pyrrolidone carboxylic acid.
By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
10 lambda chain V-II region TRO.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                             111 AA
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                                                                                                                1; Mismatches
                                            97.1%;
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              Query Match
Best Local Similarity 85.77
Conservative 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                              606 DISKRPS 612
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52 DVTKRPS 58
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                          1 DVSKRPS 7
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD RES
DISULFID
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SEQUENCE
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Q6P107
AC G6P107
DD G6-D
DD G5-D
DD G6-D
DD G7-D
DD G
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Type IIS restriction enzyme R protein (MBOIR).
OrderedLocusNames=HP1366;
Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                               91.4%; Score 32; DB 2; Length 236; 85.7%; Pred. No. 69; ive 1; Mismatches 0; Indels
InterPro; IRR00110; Ig-like.
InterPro; IRR001110; Ig-like.
InterPro; IRR003599; Ig.
InterPro; IRR003596; Ig_MG.
InterPro; IRR003596; Ig_WHC.
InterPro; IRR003596; Ig_W.
Ram, PR07664; Cl-set; 1.
SMART; SM00409; IG, 2.
SMART; SM00406; IGV; 1.
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92UM7Q

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DOI=10.1128/JB.185.18.5591-5601.2003; Nelson K.E., Pleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E., Elsen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J., Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J., Complete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83."; Bacteriol. 185:5591-5601(2003).
                                                      OTMUS6

OTMUS6,

OTMU
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SEQUENCE 130 AA; 14455 MW; 3F2B1F64F23E5805 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22829867; PubMed=12949112;
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Best Local Similarity 71.49;
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107 DISRRPS 113
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Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Waldman J.F., Fujii C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=79062503; PubMed=102365; DOI=10.1016/0005-2795(78)90598-6; MEDLINE=79062503; PubMed=102365; DOI=10.1016/0005-2795(78)90598-6; Menn B.L., Chiu Y.-Y.H., Humphrey R.L., Poljak R.J.; Andio acid sequence of the human myeloma lambda chain Win."; Biochim. Biophys. Acta 837:9-21(1978).
-!- MISCELLANEOUS: This is a Bence-Jones protein.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR, A01978; L2HUWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.6%; Score 31; DB 1; Length 111;
85.7%; Pred. No. 53;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               423 AA; 50047 MW; 9086E51C8FE4E58E CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
19 lambda chain V-II region WIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 AA
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                                                                                                                                                                                                                                                                        EMBL; AE000637; AAD08410.1; -.
PIR; F64690; F64690.
                                                                                                                                                                                                                                                                                                                                 TIGR; HP1366; -.
InterPro; IPR003615; HNH nuc.
SMART; SM0507; HNHC; 1.
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                       pylori.";
Nature 388:539-547(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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|:|||||
71 DMSKRPS 77
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P01712;
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AC P01712 H

DT 21-JUL

DT 21-JUL

DE 19 1-JUL

DE 19 1-JU
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88.6%; Score 31; DB 2; Length 130; 71.4%; Pred. No. 63; 1.4%; Pred. 2; Mismatches 0; Indels

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A Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Bikins T., Engels R., Wang S., Nichaen C.B., Butler J., Endrizzi M., A Dui D., Ianakiev P., Padersen D., Nelson M., Washburne M., Endrizzi M., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., A Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D., Kroken S., Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D., Kroken S., Argotofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Araden O., Plamann M., Seiler S., Dunlap J., Freiteg M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B., Martyle D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freiteg M., Martyle D.O., Alex L.A., Mannhaupt G., Birren B., Martyle D.O., Alex L.A., Mannhaupt G., Birren B., Martyle D.O., Alex L.A., Mannhaupt G., Birren B., Martyle D.O., Alex D.O., Alex L.A., Mannhaupt G., Birren B., Martyle D.O., Alex 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 0:0-0(2003).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Fungi, Ascomycota; Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora,
                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                  233 AA.
                                                                                                                                                                    Created)
                                  PRT;
Q7S4H3 PRELIMINARY;
Q7S4H3;
Q7S4H3;
Q1-MAR-2004 (TrEMBLrel. 26, Lic
01-MAR-2004 (TrEMBLrel. 26, Lic
01-MAR-2004 (TrEMBLrel. 26, Lic
Hypothetical protein.
Name=NCU02220.1;
Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Gaps

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DVDKRPS 58 1 DVSKRPS 7

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88.6%; Score 31; DB 2; I
85.7%; Pred. No. 2.5e+02;
Predicted nucleoside-diphosphate sugar epimerase.
ORFNames=BF1430;
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MEDLINE=22608306; PubMed=12692562;
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Matches 6; Conservative
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Best Local Similarity
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Q828G3;
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R Neuroscience 121:935-945(2003).

R ZFIN; ZDB-GENE-030319-2; p2rx2.

R ZFIN; ZDB-GENE-030319-2; p2rx2.

R GO; GO:0005503; C:1196h-harvesting complex (sensu viridiplantae); IEA.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0005216; F:10n channel activity; IEA.

R GO; GO:0016978; F:10pcate-protein ligase B activity; IEA.

R GO; GO:0006911; F:neceptor activity; IEA.

R GO; GO:0006911; F:neceptor activity; IEA.

R GO; GO:0006911; P:nerapy pathways; IEA.

R GO; GO:0006911; P:nerapy pathways; IEA.

R InterPro; IPR001429; P2X_receptor; IEA.

R Pfam; PF000864; P2X_receptor; I.
                                                                         .; IEA.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ATP-gated ionocropic P2X receptor subunit 2.
Name-p21x2; Synonyms-p2x15;
Name-p21x2; Synonyms-p2x16;
Barachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
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                     preliminary data.

EMBL, AABX0100336; EAA30397.1; -.

GO, GO:0030289; C:periplasmic space (sensu Gram-negative Bact. ..

GO, GO:0015035; F:protein disulfide oxidoreductase activity; IEA.

InterPro; IPR01085; DSBA.

InterPro; IPR010986; D8bA_insertion.

Pfam; PF01323; DSBA; 1.

Hypothetical protein.

SEQUENCE 233 AA; 25367 MW; 50B8F4A369168929 CRC64;
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                                                                                                                                                                                                                                                                                                        Query Match 88.6%; Score 31; DB 2; Length 233; Best Local Similarity 85.7%; Pred. No. 1.2e+02; Matches 6; Conservative 1; Mismatches 0; Indels
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Matches 6, Conservative
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NCBI TaxID=7955;
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25-OCT-2004
25-OCT-2004
25-OCT-2004
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Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N., Kuwahara T., Yamashita A., Hatrori M., Hayashi T., Ohnishi Y.; Hattori M., Hayashi T., Ohnishi Y.; Genomic analysis of Bacteroides fragilis reveals extensive DNA inversions regulating cell surface adaptation."; Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004). EMBL, AP006841; BAD48181.1. SEQUENCE 402 AA, 45596 MW; 2D56A6DAF87797CC CRC64;
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MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
metabolites.";
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
Dacteroides fragilis.
Bacteria; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
NCBI_TaxID=817;
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PROSTTE; PSO0086; CYTOCHROME P450, UNKNOWN 1.
COMPLETE PRO10086; CYTOCHROME P450, UNKNOWN 1.
SEQUENCE PRO10096; Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 486 AA; 53354 MW; A728B74F6592E265 CRC64;
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-- SIMILARITY: Belongs to the cytochrome p450 family. BMIDARITY: Belongs to the cytochrome p450 family. BMIDARITY: BAC74417.1;

GO, GO:0004497; F:monooxygenase activity; IEA. GO; GO:006618; P:electron transport; IEA. InterPro; IPR002397; BP450.

InterPro; IPR001128; Cytochrome_P450.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUNA2-2004 (TrEMBLrel. 26, Last annotation update)
Putative cytochrome P450.
Name=cyp24; OrderedLocusNames=SAV6706;
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RESULT 8 Q7SZL9

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Gaps

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Galdagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
A Jaffe D., FitzHugh M., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
B. Linakiev P., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
A Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
A Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
A Kandl M., Naylor J., Thomann N., Barrett R., Gnerre S.,
A Kandl M., Kamwysselis M., Maucell E., Belke C., Rudd S., Frishman D.,
A Kandl M., Kamwysselis M., Maucell E., Bielke C., Rudd S., Frishman D.,
A Kandl M., Kamwysselis M., Maucell E., Bielke C., Rudd S., Frishman D.,
A Cogoni C., Macino G., Catcheide D., Li W., Pratt R.J., Osmani S.A.,
A DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
A DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
A Parden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
A Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
The Genome Sequence of the Filamentous Fungus Neurospora crassa."; STRAIN=C4;
PubMed=14665450; DOI=10.1128/EC.2.6.1151-1161.2003;
Catlett N.L., Yoder O.C., Turgeon B.G.;
"Whole-genome analysis of two-component signal transduction genes in Gaps Nature 0:0-0[2003].
-1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
EMBL; AABX01000022; EAA35484.1; -. SEQUENCE 728 AA; 79550 MW; 05A688EBD3850B79 CRC64; Neurospora crassa. Eukaryota; Fungi; Ascomycota; Perizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora. ö Cochliobolus heterostrophus (Drechslera maydis), Eukaryota; Pungi; Ascomycota; Pezizomycotina; Dothideomycetes; Pleosporales; Pleosporaceae; Cochliobolus. 88.6%; Score 31; DB 2; Length 728; 85.7%; Pred. No. 3.8e+02; ive 0; Mismatches 1; Indels Created)
Last sequence update)
Last annotation update) G6SLD6 PRELIMINARY, PRT, 1292 AA. GSLD6; O-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) PRT; Putative histidine kinase HHK11p. 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, PRELIMINARY; Local Similarity 85.7 .. 428 DVSQRPS 434 336 DASKRPS 342 1 DVSKRPS 7 1 DVSKRPS 7 Predicted protein. Name=NCU00559.1; SEQUENCE FROM N.A. NCBI_TaxID=5141; Name=HHK11; RESULT 11 Q7SF90 ID Q7SF90 AC Q7SF90; Query Match Best Loca Matches RESULT 12 ò a

RT fungal pathogens.";

Eukaryotic Cell 2:1151-1161(2003).

C. -- SIMILARITY: Conteains 1 histidine kinase domain.

BR GO: GO: 0016020; C: membrane; IEA.

BR GO: GO: 0016020; C: membrane; IEA.

BR GO: GO: 0016524; F: APP binding; IEA.

BR GO: GO: 0016301; F: F: DNA binding; IEA.

BR GO: GO: 0016301; F: R: DNA binding; IEA.

BR GO: GO: 0016301; F: R: DNA binding; IEA.

BR GO: GO: 0016301; F: R: DNA binding; IEA.

BR GO: GO: 0010156; F: R: Component response regulator activity; IEA.

BR GO: GO: 0000160; P: R: Component asymmetry of the component response regulator activity; IEA.

BR GO: GO: 0000160; P: R: Component asymmetry of the component asymmetry and the component asymmetry of the component asymmetry of the component asymmetry of the component asymmetry and the component asymmetry of the component asymmetry and the co ö ö Gaps Gaps Ashbya gossypii (Yeast) (Eremothecium gossypii). Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Bremothecium. NCBI_TaxID=33169; ö STRAIN-ATCC 10895;
Voegeli S.E., Dietrich F.S., Brachat S., Lerch A., Gaffney T.,
Voegeli S.E., Dietrich F.S., Brachat S., Lerch A., Gaffney T.,
Shilippen P.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016815; AASS0638.1; -.
AGD; ABL133C; -.
SEQUENCE 1766 AA; 179132 MW; BEC73A1CF69F2EA3 CRC64; ö Query Match 88.6%; Score 31; DB 2; Length 1292; Best Local Similarity 85.7%; Pred. No. 6.9e+02; Matches 6; Conservative 0; Mismatches 1; Indels / Match 88.6%; Score 31; DB 2; Length 1766; Local Similarity 85.7%; Pred. No. 9.6e+02; les 6; Conservative 1; Mismatches 0; Indels Q75E06, 05-JUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) PRELIMINARY; |||:||| 1445 DVSERPS 1451 45 DVDKRPS 51 1 DVSKRPS 7 1 DVSKRPS 7 SEQUENCE FROM N.A. ORFNames=ABL133C; ABL133Cp. Query Match Q75E06 RESULT 13 Q75E06 Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and versican.

CATALYTIC ACTIVITY: Cleaves aggrecan at the 1838-Glu-|-Ala-1839 site and versican at the 1428-Glu-|-Ala-1429 site.

1- COPACTOR: Binds 1 zinc ion per subunit (By similarity).

1- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).

2. ISUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).

3. Event-alternative splicing; Named isoforms-3;

3. Name=1; Synonyms=ADAMTS-9B;

3. Isold=Q9P2N4-1; Sequence=Displayed;

3. Isold=Q9P2N4-1; Sequence=USP 007548, USP 007549;

3. Isold=Q9P2N4-1; Sequence=USP 007548, USP 007549;

3. Isold=Q9P2N4-1; Sequence=USP 00600;

3. Isold=Q9P2N4-2; Sequence=USP 00600;

3. Isold=Q9P2N4-2; Sequence=USP 00600;

3. Isold=Q9P2N4-2; Sequence=USP 00600;

4. Isold=Q9P2N4-2; Sequence=USP 00600;

5. Isold=Q9P2N4-2; Sequence=USP 00600;

6. Isold=Q9P2N4-2; Sequence=USP 00600;

7. Isold=Q9P2N4-2; Sequence=USP 00600;

8. EXPRESSED SPECIFICITY: Highly expressed in all fetal tissues.

8. Expressed in a number of adult tissues with highest expression in head of the context of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heart, placenta and skeletal muscle.
DOMAIN: The spacer domain and the TSP type-1 domains are important
for a tight interaction with the extracellular matrix (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a novel member of the ADAM-TS/Metallospondin gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20181126; PubMed=10718198;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XVI. The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro.";
DNA ROS F65-73 (2000).
-I- FUNCTION: Cleaves the large aggregating proteoglycans, aggrecan and versican.
                                                                                                                                                                                                            metalloproteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1), AND FUNCTION.
MEDLINE=22513925; PubMed=12514189; DOI=10.1074/jbc.M211009200;
Somerville R.P., Longpre J.-M., Jungers K.A., Engle J.M., Ross M.,
Evanko S., Wight T.N., Leduc R., Apte S.S.;
"Characterization of ADAMTS-9 and ADAMTS-20 as a distinct ADAMTS
subfamily related to Caenorhabditis elegans GON-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
DOMAIN: The ancillary domains, including the TSRs domain, are
required for specific extracellular localization and for its
                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   versicanase and aggrecanase activities.

PTM: The precursor is cleaved by a furin endopeptidase (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20396138; PubMed=10936055; DOI=10.1006/geno.2000.6246; Clark M.E., Kelner G.S., Turbeville L.A., Boyer A., Arden K.A. Maki R.A.; a novel member of the ADAM-TS/Metallospondin gene f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the peptidase M12B family.
-!- SIMILARITY: Contains 1 disintegrin-like domain.
-!- SIMILARITY: Contains 1 GON domain.
-!- SIMILARITY: Contains 15 TSP type-1 domains.
                                                                     A19-PART AND CONTROLL OF CONTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 159-1935 FROM N.A. (ISOFORM 2).
                                            PRT; 1935 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 278:9503-9513(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 3) TISSUE=Fetal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics 67:343-350(2000).
                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
                                                   HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      +
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                     (Potential). (Potential). (Potential).
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.) (Potential).
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By similarity.
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Disintegrin-like.
TSP type-1 1.
Cys-rich.
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135 type-1 3

135 type-1 5

135 type-1 5

135 type-1 6

135 type-1 1

135 type-1 1
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11555
11611
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Page
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us-10-614-959-14.rup

COOT 67.65.07

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N-linked (GlcNAc. . .) (Potential).
CLVTCGKGH -> VRWEGCYFP (in isoform 3).
/FTId=VSP_005499.
                         Missing (In lacform 3).

/FTIG=VSP 005500.

CSVTCG -> VPSWEL (in isoform 2)
/FTIG=VSP 007548.

Missing (In isoform 2).
/FTIG=VSP 007549.

/FTIG=VSP 007549.
                                                                                    S -> G (in Ref. 1).
P -> S (in Ref. 1).
D -> G (in Ref. 2).
F -> L (in Ref. 1).
V -> G (in Ref. 3).
6 MW, FD3D51E88300A3C6 CRC64;
                                                                                                                                   216556
                                                                                    46
96
182
367
1117
                               1935
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1935 AA;
 1806
1064
                               1073
                                                1624
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CONFLICT
CONFLICT
SEQUENCE
  CARBOHYD
                                            VARSPLIC
            VARSPLIC
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                                                                 VARSPLIC
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Gaps ö 88.6%; Score 31; DB 1; Length 1935; 100.0%; Pred. No. 1.18+03; 1ve 0; Mismatches 0; Indels Query Match Best Local Similarity 100.

1 DVSKRP 6

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|||||| 1596 DVSKRP 1601

STANDARD; BFR1 MAGMG 050171; RESULT 15
BREAL MAGMG
BAC OS0171;
DT 15-UULDT 05-UULDT 05-UULDR NAME=bACK
OC RACGOS
OX NCB1 TE
RN [1] TRN [1

164 AA

Magnetospirillum magnetotacticum (Aquaspirillum magnetotacticum) Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales; Rhodospirillaceae, Magnetospirillum. 15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Bacterioferritin subunit 1 (BFR 1). • Name=bfr1;

NCBI_TaxID=188;

SEQUENCE FROM N.A.

MEDLINE-98072426; PubMed=9409768; DOI=10.1016/S0378-1119(97)00424-1; Bertani L.E., Huang J.S., Weir B.A., Kirschvink J.L.; Bertani L.E., Huang J.S., Weir B.A., Kirschvink J.L.; Evidence for two types of subunits in the bacterioferritin of Magnetospirillum magnetotacticum."; Magnetospirillum magnetotacticum."; ele PUNCTION: May perform analogous functions in iron detoxification and storage to that of animal ferritins (By similarity).

monomer (Potential).
---SUBUNIT: Oligomer of 24 identical subunits (By similarity).
---MISCELLANBOUS: The di-iron binding site functions as active site where iron ions are oxidized from iron(II) to iron(III) before they are stored (By similarity).
---SIMILARITY: Belongs to the bacterioferritin family.
----SIMILARITY: Contains 1 ferritin-like diiron domain.

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InterPro; IPR002024; Bacterioferritin. InterPro; IPR009078; Ferritin/RR_like. InterPro; IPR008331; Ferritin Dps. InterPro; IPR009040; Ferritin_like. Pfam: PF00210; Ferritin; Ilke. PRINTS; PR00601; BACFERRITIN.

EMBL; AP001959; AAC91253.1; -.

Iron 1 (By similarity).
Iron (heme axial ligand) (Potential).
Iron 1 (By similarity).
Iron 2 (By similarity). Probom, PD002269, Bacterioferritin; 1.
TIGREAMS; TIGR00754; bfr; 1.
PROSITE; PS00549; BACTERIOFERRITIN; 1.
PROSITE; PS0055; FERTIN LIKE; 1.
Heme; Iron; Iron storage; Mecal-binding. 18491 MW; 18 51 51 51 12 54 13 13 13 13 METAL SEQUENCE METAL METAL METAL METAL METAL METAL METAL

Gape ö Score 30; DB 1; Length 164; Pred. No. 1.4e+02; 1; Mismatches 0; Indels 85.7%; 5; Conservative Best Local Similarity Matches 5; Conserv Query Match

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Search completed: October 14, 2005, 16:19:57 Job time : 48.5938 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

using sw model protein search, protein ĕ

October 14, 2005, 15:51:19 ; Search time 84.5625 Seconds (without alignments) 50.310 Million cell updates/sec Run on:

US-10-614-959-15 58 Title: Perfect score:

1 AAWDDSLSEFL 11 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A_Geneseq_16Dec04;*
1: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aav79073 Anti-fact		· LO	4	8	N	~	6	m	N	н	ß	٠	-	~	9	m	0 Neuroki	_			. ~	TNF DYC	֓֞֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓	_	•
Desc	Aav	Aars	Aaw	Aau	Aau	Aau0261	Aau0262	Aauc	Aaw1988	Aau0254	. Aau0255	Aau0258	Aau0260	Adq3430	Adq3431	Abp4591	Adq9674	Adg3	Ada3	Adq3430	Abp4591	Ada9674	Adagans	Adea	Ada3	
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ID	AAY7907	AAR8008	AAW9548	AAU0254	AAU02558	AAU0261	AAU0262	AAU02629	AAW19883	AAU02542	AAU02551	AAU02585	AAU02606	ADG34301	ADG3431	ABP4591	ADG9674	ADG34310	ADG34306	ADG34303	ABP45915	ADG96742	ADG98057	ADE83862	ADG34308	
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Length	11	104	104	109	110	110	110	110	111	111	111	111	111	242	242	243	243	243	243	244	245	245	245	4	245	
Query Match	12	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
Score	58	28	28	58	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	58	58	
Bult No.	1	7	٣	4	S	9	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	

Abp45902 Human BLy Abp45906 Human BLy Adg96733 Single ch Adg96729 Single ch Adg96729 Single ch Adp45421 Human BLy Abp45871 Human BLy Abp45817 Human BLy Adg96711 Human BLy Adg96715 Single ch Adg96418 Single ch Adg96418 Single ch Adg96429 Single ch Adg96515 Single ch Adg96515 Single ch	Adg96523 Single ch Ade83874 Chemokine
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ALIGNMENTS

AAY79073 standard; peptide; 11 AA.

AAY79073;

12-JUN-2000 . (first entry)

Anti-factor IX/IXa antibody L chain V domain CDR3 amino acid sequence

Complementarity determining region 3, CDR3; antibody, Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; light chain; arterial thrombosis; unstable angina; post myocardial infarction; coronary arter; bypass graft; CABG; stroke; tumour growth; metastesis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC. AAY79073
ID AAY77
XX
AC AAY77
XX
DT 12-JJ
XX
DX AAT1-JJ
XX
DX AAT1-JJ
XX
COMP
KW ATCE:
KW ATC

Homo sapiens.

WO200012562-A1.

09-MAR-2000.

99WO-US019453. 26-AUG-1999;

98US-0098233P. 99US-0122767P. 28-AUG-1998; 03-MAR-1999;

(GETH) GENENTECH INC.

Kirchhofer D; Judice JK, Навв РЕ, Devaux B, Eaton DL, Adams CW, Suggett S;

#PI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

Claim 8; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 3 (CDR3) of the light chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXA a vitamin K dependent plasma serime procease that participates in the blood coagulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

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the treatment or prophylaxis of thrombotic or cosquiopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypase graft (CABG), percutaneous transluminal coronary angioplasty (PTCA), stroke, tumour growth, invasion or metastessis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Production of catalytic antibodies displayed on phage - by generating gene library of antibody-derived domains and expressing it in phage
                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "complimentarity determining region 1"
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                                                                                                                                                                                                                                                                                                                                                                                     Light chain; RT3; human; catalytic antibody; bacteriophage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "complementarity determining region
                                                                                                                                                             Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chiswell D, Darsley MJ, Titmas RC, Williams RO;
                                                                                                                                                             100.0%; Score 58; DB 3;
100.0%; Pred. No. 0.0022;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                               Human derived light chain RT3 phage antibody.
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.e= "framework region 2"
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/note= "framework region 4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                             AAR80087 standard; protein; 104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94WO-US003420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94WO-US003420
                                                                                                                                                                                                                                                                                                                                           23-MAY-1996 (first entry)
                                                                                                                                                     Query Match
Best Local Similarity luv.
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Martin MT,
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IGEN-) IGEN INC
                                                                                                                                          Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kenten JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith RG,
                                                                                                                                                                                                                                                                                                                    AAR80087;
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The invention relates to methods for producing catalytic antibodies displayed on a phage. The method comprises: (a) generating a gene library of antibody-derived domains; (b) inserting coding for the domains into a phage expression vector; and (c) isolating the catalytic antibodies. The phage expression vector incorporates a histidine peptide in tandem with a myc peptide. The catalytic antibodies can be isolated by preparing an antigen, optionally immunising an animal with the antigen; generating a library of VH and VL domains from the immunised animal; cloning the VH and VL domains from the immunised animal; cloning the VH and VL domains into a phage expression vector to generate phage display
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Production of catalytic antibodies displayed on bacteriophages - comprises generating a gene library of antibody-derived domains inserting coding into a phage expression vector and isolating the catalytic antibodies.
                                                                                                                                                                  ö
    AAT04634 encodes AAR80087 human derived light chain RT3 phage antibody. The DNA was used in the prepn. of catalytic antibody (CA) producing bacteriophage. The CAs can be used to activate/deactivate a biological function in an animal by enhancing the rate of cleavage, or formation of a specific bond within a mol. in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                     Catalytic; antibody; phage display; immunising; phage expression vector; prodrug; scFV; RT3.
                                                                                                                                                                    Gарв
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                                                                                                                                                                                                                                                                                                                                                                                                          Human-derived RT3 phage antibody light chain genetic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Martin MT;
                                                                                                                                 100.0%; Score 58; DB 2; Length 104; 100.0%; Pred. No. 0.023; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fitzgerald K, Darsley MJ, Williams RO, Smith R, Kenten JH, Chiswell D, Mccafferty J, Titmas RC;
                                                                                                                                                                                                                                                                                                                  AAW95485 standard; protein; 104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Fig 20B; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-00273146
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                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                     1 AAWDDSLSEFL 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHISWELL D.
DARSLEY M J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITMAS R C.
MARTIN M T.
KENTEN J H.
SMITH R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-105036/09.
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                                                                                                          Sequence 104 AA
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(CHIS/)
(DARS/)
(TITM/)
(MART/)
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Disclosure; Fig 20; 133pp; English

vectors.

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antibodies; selecting phage display antibodies which bind specifically to the antigen; screening the selected phage display antibodies for catalytic activity to substrate; and isolating the catalytic antibodies, where the phage expression vector incorporates a histidine peptide in tandem with a myc peptide. The processes are used to produce catalytic antibodies, which can be used for in vivo activation of a prodrug. Sequences AAW95484-489 represent genetic sequences of heavy and light chains of RT3 specific phage antibodies selected from a naive human phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody library
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Sequence 104 AA;

100.0%; Score 58; DB 2; Length 104; 100.0%; Pred. No. 0.023; 1.1ve 0; Mismatches 0; Indels Local Similarity 100. 1 AAWDDSLSEFL 11 83 AAWDDSLSEFL 93 Query Match Matches g ઠે

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Gaps

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RESULT 4

AAU02544 standard; protein; 109 AA. AAU02544; Anti-adipocyte monoclonal antibody light chain, FAT 31

(first entry)

29-AUG-2001

Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.

Homo sapiens

#0200127279-A1.

19-APR-2001

11-OCT-2000; 2000WO-GB003900

12-OCT-1999;

(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Vaughan TJ Edwards BM, Main SH,

Claim 1; Page 128-129; 182pp; English.

diseases

WPI; 2001-282031/29. N-PSDB; AAS03444.

Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases

Claim 1; Page 120; 182pp; English.

AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
cobesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
catectable label such as radiolabel, fluorescent or chemical group and
used in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intra-

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Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                     Gaps
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                                                                                                                                                                                                        fat;
                                    Length 109;
                                  Score 58; DB 4; Length 10; Pred. No. 0.024; 0; Mismatches 0; Indels
                                                                                                                                                                                                    Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.
                                                                                                                                                                                    Anti-adipocyte monoclonal antibody light chain, FAT 44.
abdominal fat associated with heart disease
                                                                                                                                                                                                                                                                                                                    (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                               AAU02558 standard; protein; 110 AA.
                                  100.0%;
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                                                                                                                                                                                                                                                                                                   12-OCT-1999; 99US-0158812P.
                                                                                                                                                                   (first entry
                                Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                               1 AAWDDSLSEFL 11
                                                                                                                                                                                                                                                                                                                                      Edwards BM, Main SH,
                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-282031/29.
                  Sequence 109 AA;
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                                                                                                                                                                   29-AUG-2001
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ID AAU
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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
cinvention. The antibodies can be used in the treatment of obesity and
cinvention. The antibodies can be used to deliver drugs or
conclude diseases. The antibodies can be used to deliver drugs or
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
confidence of adipocyte artigles. The antibodies may be labeled with a
cused in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
contraction than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intracontraction. ö Gapa ô Sequence 110 AA;

Query Match 100.0%; Score 58; DB 4; Length 110; Best Local Similarity 100.0%; Pred. No. 0.024; Matches 11; Conservative 0; Mismatches 0; Indels

fat;

unti-adipocyte monoclonal antibody light chain, FAT 112. Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.

29-AUG-2001 (first entry)

AAU02627;

(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Edwards BM, Main SH,

99US-0158812P

2-0CT-1999;

11-OCT-2000; 2000WO-GB003900

40200127279-A1 Homo sapiens.

19-APR-2001.

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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
obesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
con be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
detectable label such as radiolabel, fluorescent or chemical group and
used in methods of diagnosis in human subjects e.g. to determine the
cycleantine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
cycleant types of fat deposits can also be produced e.g. intra-
condificerent types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                           Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
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                                                                                                                      AAU02612 standard; protein; 110 AA
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Best Local Similarity 100.
Matches 11; Conservative
                    90 AAWDDSLSEFL 100
1 AAWDDSLSEFL 11
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consistency and monocortain antibody heavy chain, light chain, and many control and monocortain antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and coesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the far mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and detectable label such as radiolabel, fluorescent or chemical group and cued in methods of diagnosis in human subjects e.g. to determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and AAU02641-AAU02748 represent the amino acid
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100.0%; Pred. No. 0.024;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 172; 182pp; English
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hes 11; Conservative
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AAU02627 standard; protein; 110 AA.

AAU02627 ID AAUC RESULT 7

AAWDDSLSEFL 100

90

1 AAWDDSLSEFL 11

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heart disease; complementarity determining region; CDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-2000; 2000WO-GB003900
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N-PSDB; AAS03529.
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                                                                                                                                              Homo sapiens.
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Vaughan TJ;

Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related

AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
clobesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
can be used as a therapeutic itself. Antibodies binding specifically to
by complement mediated lysis. The antibodies binding specifically to
by complement mediated lysis. The antibodies binding specifically to
captioned as radiolabel, fluorescent or chemical group and
detectable label such as radiolabel, fluorescent or chemical group and
category antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposite can also be produced e.g. intraabdominal fat associated with heart disease

Sequence 110 AA;

Gaps ö Query Match 100.0%; Score 58; DB 4; Length 110; Best Local Similarity 100.0%; Pred. No. 0.024; Matches 11; Conservative 0; Mismatches 0; Indels Best Loca Matches

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RESULT 9

AAW19883 standard; protein; 111 AA. AAW19883

CEA-specific antibody CEA1, CEA2, CEA3 VL sequence

07-DEC-1997 (first entry)

Carcinoembryonic antigen; CEA; human; antibody; scFv; tumour marker; lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.

Homo sapiens

Location/Qualifiers Key Region

23. .35
/label= CDR1
/note= "complementarity determining region 1"

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This polypeptide sequence comprises the light chain variable region (VL) of human carcinoembryonic antigen (hCEA)-specific antibodies CEA1, CEA2 and CEA1, WA (AAT7213-35) gene sequences were obtained for anti-hCEA antibodies CEA1(see AAW19876-85). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 -8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-83 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL variantes (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Specific binding members for human carcinoembryonic antigen - bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing cancer.
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50. .56
/label= CDR2
/note= "complementarity determining region 2"
/label= CDR3
/note= "complementarity determining region 3"
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96GB-00021295
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Osbourn JK, Allen DJ,
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                                                                                                                                                                                                                                                                                                                                                                                                             09-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAY-1996;
11-OCT-1996;
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                                                                                                               Region
       Region
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Anti-adipocyte monoclonal antibody light chain, FAT 30 AAU02542 standard; protein; 111 AA. (first entry) 90 AAWDDSLSEFL 100 1 AAWDDSLSEFL 11 29-AUG-2001 AAU02542; RESULT 10 AAU02542 ઠ 셤

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Antibody; adipocyte; heavy chain; 11ght chain; obesity; heart disease; complementarity determining region; CDR. 40200127279-A1 domo sapiens

19-APR-2001.

fat;

WPI; 2001-282031/29.

N-PSDB; AAS03451

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(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                           (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                         Claim 1; Page 118-119; 182pp; English.
                                                                                                                                                                                                                                                                                  AAU02551 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-2000; 2000WO-GB003900
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     11-OCT-2000; 2000WO-GB003900.
                99US-0158812P.
                                                                                                                                                                                                                                                                                                        29-AUG-2001 (first entry)
                                                                                                                                                                                                                         Local Similarity 100
                                                                                                                                                                                                                                                   90 AAWDDSLSEFL 100
                                                                                                                                                                                                                                           1 AAWDDSLSEFL 11
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                                       Main SH,
                                                 WPI; 2001-282031/29.
                                                       N-PSDB; AAS03442
                                                                                                                                                                                                          Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                           WO200127279-A1
                12-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                       Edwards BM,
                                                                                                                                                                                                                                                                                             AAU02551;
                                                                              diseases,
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                                                                                                                                                                                                                                                                       RESULT 11
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11-OCT-2000; 2000WO-GB003900
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 111 AA;
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                                                                                                                                              diseases
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sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
cobesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
cor an be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
complement mediated lysis. The antibodies may be labeled with a
detectable label such as radiolabel, fluorescent or chemical group and
used in methods of diagnosis in human subjects e.g. to determine the
copresence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 58; DB 4; Length 111; 100.0%; Pred. No. 0.025;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-adipocyte monoclonal antibody light chain, FAT 37.
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                                                                                                                                                                       Vaughan TJ
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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
cinvention. The antibodies can be used in the treatment of obesity and
cinvention. The antibodies can be used to deliver drugs or
pro-trugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
considered the presence of adiagnosis in human subjects e.g. to determine the
cused in methods of diagnosis in human subjects e.g. to determine the
considered the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
considered than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
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Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU02585 standard, protein; 111 AA.
                                                                                                       Claim 1; Page 124; 182pp; English.
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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
twention. The antibodies can be used in the treatment of obesity and
obesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the far mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
can be used as therapeutic itself. Antibodies binding specifically to
by complement mediated lysis. The antibodies binding specifically to
by complement mediated lysis. The antibodies binding specifically to
catipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies of destroy the cells
categories of a back as radiolabel, fluorescent or chemical group and
categories of adipocyte antigen on the surface of an adipocyte to determine the
categories can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
contained the present of fat deposite can also be produced e.g. intra-
abdominal fat associated with heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU02606 standard; protein; 111 AA
              Claim 1; Page 146; 182pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-AUG-2001 (first entry)
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Matches 11; Conservative
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100.0%; Score 58; DB 4; Length 111; 100.0%; Pred. No. 0.025; ative 0; Mismatches 0; Indels

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can be used as a therapeutic itself. Antibodies binding specifically to adjocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adjocyte antigen on the surface of an adjocyte to detect or determine the presence or level of adjocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients of the unundergoing surgery to remove axcess fat. Antibodies for different types of fat deposits can also be produced e.g. intrasabdominal fat associated with heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibody that specifically binds neurokinin B, useful for preparing a composition for treating or preventing hypertension or preeclampsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel antibody specifically binding neurokining. B. An antibody of the invention has hypotensive, and gynaecological activity, and may have a use in gene therapy. The antibody is useful for preparing a composition for treating or preventing hypertension or preclampsia. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody; neurokinin B; hypotensive; gynaecological; gene therapy; hypertension; pre-eclampsia; NKB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADG34301 standard; protein; 242 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2002; 2002US-0383802P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                         91 AAWDDSLSEFL 101
                                                                                                                                                                                                                                                                                                                                                                                 1 AAWDDSLSEFL 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-053456/05.
N-PSDB; ADG34282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                         Sequence 111 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADG34301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

99US-0158812P.

12-OCT-1999;

11-OCT-2000; 2000WO-GB003900

19-APR-2001

Vaughan TJ

Edwards BM, Main SH, WPI; 2001-282031/29. N-PSDB; AAS03506. Claim 1; Page 159; 182pp; English.

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221 AAWDDSLSEFL 231

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New antibody that specifically binds neurokinin B, useful for preparing a composition for treating or preventing hypertension or preeclampsia.
                                                                                        antibody; neurokinin B; hypotensive; gynaecological; gene thexapy; hypertension; pre-eclampsia; NKB.
                                                                                                                                                                                                                                                                                                       Claim 2; SEQ ID NO 40; 127pp; English.
                 ADG34317 standard; protein; 242 AA.
                                                                        Neurokinin B antibody SEQ ID NO:40,
                                                                                                                                                                          29-MAY-2003; 2003WO-US016802.
                                                                                                                                                                                            30-MAY-2002; 2002US-0383802P.
                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
                                                      26-FEB-2004 (first entry)
                                                                                                                                                                                                                                  Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                 WPI; 2004-053456/05.
N-PSDB; ADG34298.
                                                                                                                                      WO2003102136-A2.
                                                                                                                                                        11-DEC-2003
                                                                                                                     Synthetic.
                                    ADG34317;
RESULT 15
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The invention relates to a novel antibody specifically binding neurokinin B. An antibody of the invention has hypotensive, and gynaecological activity, and may have a use in gene therapy. The antibody is useful for preparing a composition for treating or preventing hypertension or preclampsia. The present sequence is used in the exemplification of the invention. Gaps ., 0 Ouery Match 100.0%; Score 50; DB 0; Length 242; Best Local Similarity 100.0%; Pred. No. 0.056; Matches 11; Conservative 0; Mismatches 0; Indels Sequence 242 AA;

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1 AAWDDSLSEFL 11

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Search completed: October 14, 2005, 16:12:42 Job time : 84.5625 secs

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Fitzgerald, Kevin
Kenten, John H.
Martin, Mark T.
Titmas, Richard C.
Williams, Richard O.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15, Appl Sequence 63, Appl Sequence 174, Appl Sequence 374, Appl Sequence 374, Appl Sequence 376, Appl Sequence 60, Appl Sequence 497, Appl Sequence 411, Appl Sequence 6, Appl Sequence 6, Appl Sequence 111, Appl Sequence 38, Appl Sequence 60, Appl Sequence 38, Appl Sequence 43, Appl Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 43, Appl Sequence 44, Appl Sequenc
                                                                                                                                                                               ; Search time 21.6562 Seconds
(without alignments)
37.917 Million cell updates/sec
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1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-273-146-63

US-08-25-266A-374

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US-08-350-260A-346

US-09-104-337A-346

US-09-104-337A-346

US-09-35-74-60

US-09-35-74-60

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US-09-35-74-60

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US-09-104-337A-497

US-09-104-337A-497

US-09-104-337A-497

US-09-115-574-60

US-09-315-574-60

US-09-315-574-38

US-09-240-274-59

US-09-240-274-59

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US-09-240-274-38

US-09-240-274-60

US-08-665-202-36

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                                                                                                                                                                                     October 14, 2005, 16:00:04;
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                          protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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58
1 AAWDDSLSEFL 11
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Maximum DB seq length: 200000000
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Score Match Length DB
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Perfect score:
Sequence:
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No.
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Sequence 13, Appl Sequence 112, App Sequence 114, Appl Sequence 5, Appli Sequence 4, Appli Sequence 4, Appli Sequence 7, Appli Sequence 60, Appl Sequence 361, Appl			11; ils 0; Gaps 0;	
US-09-315-574-39 US-08-211-202-113 US-08-211-202-114 US-08-665-202-5 US-09-315-574-5 US-09-915-574-5 US-09-956-086-4 US-09-956-087-4 US-09-986-44-7 US-09-983-42-7 US-09-983-42-7 US-09-983-42-7 US-09-983-42-7 US-09-383-584-7 US-09-383-584-7 US-09-383-584-40 US-09-315-574-40 US-09-350-260A-361 US-08-350-260A-361 US-08-350-260A-361 US-08-350-260A-361	ALIGNMENTS	W. W. In itel Y. Anti-Factor IX/IXa Antibodies 1: US/09/383,667 08-26 08-26 1: US 60/098,233 08-28 1: US 60/122,767	; Score 58; DB 4; Length ; Pred. No. 0.00037; 0; Mismatches 0; Indel	773146 1 1 . J.
1111122255833111111111111111111111111111		us/09: i.a w. iitte iitte cevin cevin lley an Ant: mER: U6 99-08-7	00	US/0827 ger , John David ichael
44444444444444		atior Camel Care Care Care Care Care Care Care Care	nilarity Conservat AWDDSLSEFL	SULT 2 Sequence 63, Application US/082731 Patent No. 5855885 GENERAL INFORMATION: APPLICANT: Smith, Rodger APPLICANT: Chiswell, David APPLICANT: Chiswell, David APPLICANT: Fitzgerald, Kevin APPLICANT: Fitzgerald, Kevin
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		667-15 No. 662 No. 6	atch cal S 11	27 2 3-273-146-6 guence 63, ent No. 58 SMERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT:
2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		RESULT 1 US-09-383-667-15 Sequence 15, Applica Sequence 15, Applica Patent No. 6624295 GENERAL INFORMATION APPLICANT: Adams, (APPLICANT: Bevaux, APPLICANT: Bevaux, APPLICANT: Judice, APPLICANT: Judice, APPLICANT: Judice, APPLICANT: Suggett, TITLE OF INVENTION FILE REFERENCE: PICTORENT APPLICATION CURRENT APPLICATION CURRENT APPLICATION CHRENT APPLICATION CHRENT APPLICATION CHRENT APPLICATION CHRENT FILING DATI EARLIER FILING DATI EARLIER PILING DATI EARLIER PILI	Query Best 1 Matche	RESULT 2 US-08-273-146-63 Sequence 63, A Patent No. 585 GENERAL INFOR APPLICANT:

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PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9525004.9

FILING DATE: 23-MAY-1996

FILING DATE: 23-MAY-1996

FILING DATE: 02-DEC-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/244,597

FILING DATE: 01-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: DAVIG W. Clough

REGISTRATION NUMBER: 36,107

REPERENCE/DOCKET NUMBER: 36,107

REPERENCE/DATAION NUMBER: 36,107
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amino acid
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Best Local Similarity 100.
Matches 11, Conservative
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US-08-652-816A-15
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60606-6402
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          TITLE OF INVENTION: The Isolation and Production of TITLE OF INVENTION: Catalytic Antibodies using Phage Technology NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: IGEN, Inc.
STREET: 1530 East Jefferson St.
CITY: Rockville
STATE: MD
COUWRY: USA
ZIP: Z0852
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Patent No. 587215
GENERAL INFORMATION:
APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Epecific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Materhall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 58; DB 2; Length 104; 100.0%; Pred. No. 0.0041;
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CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
CONDUTER READABLE FORM:
MEDIUN TYPE: Floppy disk
COMPUTER: PLOPPY disk
COMPUTER: PLOPPY DISK
COMPUTER: PARTINE STATEM: PC-DOS/WS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FLING DATE: 23-MAY-1996
FROR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FLING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
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MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin DATA:
APPLICATION NUMBER: US/08/273,146
FILING DATE: 14-JUL-1994
CLLASSIFICATION NUMBER: US/08/273,146
FILING DATE: NUMBER: 33,771
REFERENCE COMPUNICATION NUMBER: 33,771
FELECOMMUNICATION INFORMATION:
TELEPHONE: 301-304-0158
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
TELEPACE: LANGE TELEPACE THE ADDITION OF SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Best Local Similarity 100.
Matches 11; Conservative
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US-08-652-816A-15
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Gaps
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APPLICANT: Williams, Samuel Cameron
APPLICANT: Williams, Samuel Cameron
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nonsein, Abuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
APPLICANT: Global Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
CUNTRY: USA
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100.0%; Score 58; DB 2; Length 111; 100.0%; Pred. No. 0.0044; Pred. No. 100.0%; Indels ive 0; Mismatches 0; Indels
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ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FLING DATE:
CLASSIPICATION: 435
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APPLICANT: Winter, Gregory Paul
APPLICANT: Williams, Samuel Cameron
APPLICANT: Williams, Samuel Cameron
APPLICANT: Williams, Samuel Cameron
APPLICANT: Wilsim, Abuva
APPLICANT: Nissim, Abuva
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: Dinding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
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COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
                                             FILING DATE: 25-Jun-1938
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 15-MAY-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GC 76893/00605
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 15-MAY-1993
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 15-MAY-1994
APPLICATION NUMBER: US 08/150,002
FILING DATE: 15-MAY-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 15-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BATCHICK!, AUGREY L.
REGISTRATION NUMBER: 28111/32372A
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
ENENTH: 11 amino acids
                               APPLICATION NUMBER: US/09/104,337A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLGY: linear SEQ ID NO: 374: US-09-104-337A-374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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MEDIUM TYPE: Floppy
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Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific binding pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESSE: Audres, L. Bartnicki
STREFT: Marehall, Geretein & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.3%; Score 46; DB 2; Length 11; 72.7%; Pred. No. 0.05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
RILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PLING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 34-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 374:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 374, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nissim, Ahuva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.3
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AAWDDSLSEFL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAWDDSLSAYV 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
US-08-350-260A-374
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Sequence 60, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REPRENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 346:
         PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/150,002
FILING DATE: 11-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; SEQUENCE DESCRIPTION: SEQ ID NO: 346: US-09-104-337A-346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 75.9
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAWDDSLAWFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AAWDDSLSEFL 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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Nissim, Ahura
Johnson, Kevin Stuart
Smith, Andrew John Hammond
Smith, Andrew John Hammond
ITTLE OF INVENTION: Methods for producing members of specific
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Geretein & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.9%; Score 44; DB 2; Length 11; 72.7%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                           PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: DCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00605
FILING DATE: 15-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, DAVIG W
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ 1D NO: 346:
ENENTH: LIA maino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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Griffiths, Andrew David
Williams, Samuel Cameron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 346, Application US/09104337A Patent No. 6492160 GENERAL INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Illinois
CCUNTRY: USA
ZIP: 60606-6402
PUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterhouse, Peter
                                       15-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                          FILING DATE: 15-MAY-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AAWDDSLSEFL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AAWDDSLAWFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: Bir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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; MOLECULE TYPE: peptide US-09-315-574-60
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Patent No. 6512097

GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:
ADDRESSEB: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Pour Embarcadero Center, Suite 1100

CITY: San Francisco
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 74.1%; Score 43; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: CALLLIANTS

ZIP: 94111-4106

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574

FILING DATE: 20-MAX-99
CLASSIPICATION 530

PRIOR APPLICATION 1995
PRIOR APPLICATION NUMBER: US 60/000,238

FILING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250

FILING DATE: 15-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250

FILING DATE: 13-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250

FILING DATE: 13-JUN-1995

PRIOR APPLICATION NUMBER: US 08/665,202

FILING DATE: 13-JUN-1996

ATTONENTY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:

NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498

REFERENCE/DOCKET NUMBER: 02307E-061410

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 60: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-665-202-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                  TYPE: amino acid STRANDEDNESS:
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Query Match

Betch Local Smilarity 100.04; Pred. No. 4.14-05;

Betch Local Smilarity 100.04; Pred. No. 4.14-05;

Betch Local Smilarity 100.04; Pred. No. 4.14-05;

Betch Separation of Conservative O. Mismatches O. Indels O. Gaps O. Mismatches O. Indels O. Indels
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NUMBER OF SEQUENCES: 60
TELEPHONE: 312-474-6300
INPORMATION FOR SEQ ID NO: 'SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                  ; TOPOLOGY: linear
US-08-350-260A-497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                               1 AAWDDSLS 8
                                                                                                                           TYPE: amino acid
STRANDEDNESS: si:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AAWDDSLS
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US-09-104-337A-339
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Sequence 497, Application US/08350260A

Patent No. 596225B

GENERAL INFORMATION:

APPLICANT: Winter, Gregory Paul
APPLICANT: Williams, Samuel Cameron
APPLICANT: Materhouse, Peter
APPLICANT: Materhouse, Peter
APPLICANT: Materhouse, Peter
APPLICANT: Massim, Ahuva
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: Methods for producing members of specific
STREET: ADDRESSE:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
CURRENT APPLICATION DATE: BC-1994
FILING DATE: B-MA'-1991
FILING DATE: F-MA'-1991
FILING DATE: 10-JUL-1991
FILING DATE: 10-JUL-1991
FILING DATE: 10-JUL-1991
FILING DATE: 10-JUL-1991
FILING DATE: 11-MA'-1992
FILING DATE: 11-MA'-1992
FILING DATE: 11-MA'-1993
FILING DATE: 11-MA'-1993
FILING DATE: 11-MAR-1993
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: WCT/GB93/00605
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 08/150,002
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 11-MAR-1994
                                                                                                                                                                                         Length 10,
                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                         Query Match 74.1%; Score 43; DB 2; Best Local Similarity 100.0%; Pred. No. 0.15; Matches 8; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
            LENGTH: 10 amino acids
                                          ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-339
                                                                                                                                                                                                                                                                                                                                                              1 AAWDDSLS 8
                                                                                                                                                                                                                                                                                                                           1 AAWDDSLS 8
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-350-260A-497
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| INPORMATION FOR EXP ID NO: 497:
| SEGURATION FOR EXP ID NO: 497:
| INPORACTION FOR EXP ID NO: 497:
| INPORTATION FOR EXP ID NO: 497:
| AMDIDISES | SECURATION |
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TYPE aning a citied

SEQUENCY: Innea

SEQUENCY: Innea

SEQUENCY: Innea

SEQUENCY: Innea

GREEL Local Similarity 100.01; Fred. No. 0.15;

Matches 8; Conservative 0, Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0, Mismatches 0; Indels 0; Gaps 0;

MANDOSIS 8

D | MANDOSIS 8

RESULT 13

SEQUENCE AST, Application US/03104337A

MANDOSIS 8

MACENDARY PROPERTY SEAD SEA

MILITARIE OF INNEALLY, Addrew David

WILLIAMS SEAD SEA

SEQUENCE AST, Application US/0310437A

SEQUENCE AST, Application US/0310437A

MACENDARY SEAD SEA

SEQUENCE AST, Application US/0310437A

MACENDARY SEAD SEA

SEQUENCE AST, APPLICATION WARRES COMPATIBLE

CONSTRUCTION SEA

SEQUENCE AST, APPLICATION WARRES COMPATIBLE

CONSTRUCTION MARKES COMPATIBLE

CONSTRUCTION WARRES COMPATIBLE

PRIOR APPLICATION WARRES COMPATIBLE

PRIOR APPLICATION WARRES COMPATIBLE

MATCHES CONSTRUCTION WARRES COMPATIBLE

MATCHES COMPATIBLE COMPATIBLE

MATCHES COMPATIBLE COMPATIBLE

MATCHES COMPATIBLE COMPATIBLE

MATCHES C
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16-00-104-137A-497

SEQUENCE DESCRIPTION: SEQ ID NO: 497;

17-14-137A-497

SECURATION TO THE TANDERS SET TO SECURD SECURD
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Job time : 21.6562 secs
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Sequence 6, Application US/08665202

Sequence 6, Application US/08665202

GENERAL INFORMATION: No. 5977322

TITLE OF INVENTION: No. 57773222

TITLE OF INVENTION: No. 577732221 High Affinity Human Antibodies to TITLE OF INVENTION: No. 577732221 High Affinity Human Antibodies to TITLE OF INVENTION: No. 577732221 High Affinity Human Antibodies to TITLE OF INVENTION: Two Promessed and Townsend and Crew LLP CORRESPONDENCE ADDRESS: Two Embarcadero Center, Eighth Floor CITY: San Francisco CONTRY: USA STATE: California

CONPUTR: San Francisco Center, Eighth Floor STATE: California

COMPUTR: Pala-1384 PORM: No. 244

MEDILATION WOMBER: US /08/665,202

COMPUTR: PatentIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA: Selesse #1.0, Version #1.30

CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: US 60/000,250

FILING DATE: 14-7UN-1995

ATTORNEY APPLICATION DATA: APPLICATION NUMBER: US 60/000,250

FILING DATE: 14-3UN-1995

ATTORNEY APPLICATION NUMBER: US 60/000,250

FILING DATE: MATHORNATION: TELEPHONE: (1415) 576-0300

INFORMATION FOR SEQ ID NO. FEREENENCE CHARACTERISTICS: LENGTH: 11 and no acide STREED CHARACTERISTICS: Lingthin The STREED CHARACTERISTICS: Lingthin The STREED CHARACTERISTICS: Ling
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                                                                                                                                                                                                      Query Match

74.1%; Score 43; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels
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i LENGTH: 11 amino acids

TYPE: amino acid

TYPE: amino acid

STRANDEDNESS: single

1 TOPOLCGY: linear

US-08-350-260A-441
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US-08-665-202-6
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Search completed: October 14, 2005, 16:22:03

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US-09-880-748-1913

US-10-293-418-1917

US-10-293-418-1917

US-09-880-748-1493

US-09-880-748-1993

US-09-880-748-1993

US-09-880-748-1993

US-09-880-748-1993

US-10-293-418-1934

US-10-293-418-1934

US-10-293-418-1934

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US-10-293-418-1934

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US-10-981-692-37

US-10-981-692-39

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US-10-981-692-39

US-09-880-748-2049

US-10-293-418-2049

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US-11-017-030-847-84
                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
  ; Search time 78.2031 Seconds (without alignments) 58.615 Million cell updates/sec
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1: \cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: \cgn2_6/ptodata/2/pubpaa/PCT_RW PUB.pep:*
3: \cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*
4: \cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*
5: \cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*
6: \cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*
7: \cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*
8: \cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*
9: \cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
11: \cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
11: \cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: \cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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19: \cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: \cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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21: \cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
22: \cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                  1859788 seqs, 416717961 residues
                                                                                October 14, 2005, 16:20:10;
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Maximum Match 100%
Listing first 45 summaries
                                                          protein search, using sw model
                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                              US-10-614-959-15
58
1 AAWDDSLSEFL 11
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Scoring table:

Searched:

Database

Perfect score:

Title:

Sequence:

OM protein -

Run on:

Sequence 1913, Ap Sequence 1917, Ap Sequence 1924, Ap Sequence 1924, Ap Sequence 1934, Ap Sequence 1934, Ap Sequence 1934, App Sequence 1934, App Sequence 27, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 21, Appl Sequence 21, Appl Sequence 2049, Ap Sequence 2049, Appl Sequence 22, Appl Sequence 23, Appl Sequence 2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 24, Appl Sequence 1927, Appl Sequence 1927, Appl Sequence 29, Appl Sequence 26, Appl Sequence 26, Appl Sequence 1926, Appl Sequence 1926, Appl Sequence 3241, Appl Description US-10-981-692-24 US-10-981-622-40 US-09-880-748-1927 US-10-293-418-1927 US-10-981-692-29 US-10-981-692-26 US-10-981-692-26 US-10-293-48-1926 US-10-293-48-1926 US-10-293-418-1926 US-10-293-418-1926 US-10-293-418-1926 В Query Match Length 100.0 100.0 100.0 100.0 100.0 100.0 100.0 Score 2643978611

ö US-10-981-692-24

Sequence 24, Application US/10981692

Sequence 24, Application US/10981692

Publication No. US20050163777A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
FILE REFERENCE: PF590P1

CURRENT APPLICATION NUMBER: US/10/981,692

CURRENT FILING DATE: 2004-11-05

PRIOR FILING DATE: 2003-05-29

PRIOR FILING DATE: 2003-05-30

NUMBER OF SEQ ID NOS: 76

SEQ ID NOS: 76

LENGTH: 242 **Gaps** ö 100.0%; Score 58; DB 18; Length 242; 100.0%; Pred. No. 0.048; Live 0; Mismatches 0; Indels FEATURE: ; OTHER INFORMATION: NO15E08 scFv US-10-981-692-24 TYPE: PRT ORGANISM: Artificial sequence Best Local Similarity 100. Matches 11; Conservative 221 AAWDDSLSEFL 231 1 AAWDDSLSEFL 11 Query Match g

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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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                                                                          TITLE OF INVENTION: ARILIDOGUED LIGG. THE CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR PILING DATE: 2001-11-16
PRIOR PLICATION NUMBER: 60/340,817
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-03-11
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-06-16
PRIOR FILING DATE: 2000-06-16
PRIOR FILING DATE: 2000-06-16
PRIOR FILING DATE: 2000-06-16
PRIOR FILING DATE: 2000-06-16
PRIOR PILING DATE: 2000-06-16
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Publication No. US20050163777A1
GENERAL INFORMATION:
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US-10-981-692-29
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Best Local Similarity 100.
Matches 11; Conservative
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US-10-293-418-1927
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US-10-981-692-29
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US-10-981-692-40

Sequence 40, Application US/10981692

Publication No. US20050163777A1

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B

TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B

TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B

CURRENT PEPLICATION NUMBER: US/10/981,692

CURRENT PEPLICATION NUMBER: PG7/US03/16802

PRIOR FILING DATE: 2003-05-29

PRIOR FILING DATE: 2003-05-29

PRIOR FILING DATE: 2003-05-30

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Petentin version 3.1

SEQ ID NO 40

LENGTH: 242
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Sequence 1927, Application US/0980748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF533

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-22

NUMBER OF SEQ ID NOS: 3239

SEQ ID NO 1927

LENGTH: 243
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100.0%; Score 58; DB 18; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial sequence
FEATURE:
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Best Local Similarity 100.
Matches 11; Conservative
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US-09-880-748-1927
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APPLICANT: Rosen et al.

TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin FILE SPERENCE: PF590P1
CURRENT APPLICANTEN WINDER: US/10/981,692
CURRENT FILING DATE: 2004-11-05
PRIOR APPLICATION NUMBER: PCT/US03/16802
PRIOR FILING DATE: 2003-05-29
PRIOR FILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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US-10-981-692-33
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US-10-293-418-1927 ; Sequence 1927, Application US/10293418 ; Publication No. US20030223996A1

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; Sequence 26, Application US/10981692
; Sequence 26, Application US/10981692
; Publication No. US2005016377741
; General information:
; TITLE OF INVENTION:
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REPERENCE: PF590P1
; CURRENT PILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: DCT/US03/16802
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR PILING DATE: 2002-05-29
; PRIOR PILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26
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                                                                       APPLICANT: Rosen et al.

TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B FILE REPERENCE: PF590P1

CURRENT APPLICATION NUMBER: US/10/981,692

CURRENT PILING DATE: 2004-11-05

PRIOR PILING DATE: 2003-05-29

PRIOR PILING DATE: 2003-05-39

PRIOR PILING DATE: 2002-05-30

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patentin version 3.1

SEQ ID NO 33

LENGTH: 243
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US-09-880-748-1926
; Sequence 1926, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; AFPLICANT: Ruben et al.
; TITLE OF INVERTOR: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
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Sequence 33, Application US/10981692
Publication No. US20050163777A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial sequence
FEATURE:
CTHER INFORMATION: NO23E01 scFv
0S-10-981-692-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: N024D01 BCFV
US-10-981-692-26
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 AAWDDSLSEFL 232
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Sequence 1926, Application US/10293418

Publication No. US/20030223996A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: 00/331,469

PRIOR PILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-25

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR PILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-17
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN Ver: 2.0
LENGTH: 245
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US-10-293-418-3241
; Sequence 3241, Application US/10293418
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Best Local Similarity 100.
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; ORGANISM: Homo sapiens
US-09-880-748-1926
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; ORGANISM: Homo sapiens
US-10-293-418-1926
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Sequence 1913, Application US/09880748

Publication No. US20030059937A1

REMEMATION:

APPLICAMT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT PELING DATE: 2001-06-15

PRIOR PELING DATE: 2000-06-15

PRIOR PELING DATE: 2000-06-15

PRIOR PELING DATE: 2000-06-15

PRIOR PELING DATE: 2000-10-17

PRIOR PELING DATE: 2001-03-16

PRIOR PELING DATE: 2001-03-16

PRIOR PELING DATE: 2001-03-16

PRIOR PELING DATE: 2001-03-16

PRIOR PELING DATE: 2001-05-25

PRIOR PELING DATE: 2001-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CAGANISM: Homo sapiens
US-09-880-748-1913
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; ORGANISM: Homo sapiens
US-09-880-748-1917
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Best Local Similarity
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Sequence 31, Application US/10981692

Publication No. US20050163777A1

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
TITLE OF INVENTION: ANGRER: US/10/981,692

CURRENT FILING DATE: 2004-11-05

PRIOR PILING DATE: 2003-05-29

PRIOR PILING DATE: 2003-05-30

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patentin version 3.1

LENGTH: 245
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                                                ## GRNERAL INFORMATION:

GRNERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT PILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-01-17

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR PILING DATE: 2001-01-17

PRIOR PILING DATE: 2001-01-17
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US-10-981-692-31
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Publication No. US20030223996A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
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US-10-293-418-3241
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Sequence 1917, Application US/09880748

Sequence 1917, Application US/09880748

Publication No. US20030059937A1

GENERAL INPORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF23

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

SPIOR APPLICATION NUMBER: 60/297,379

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

SOFTWARE: PARENT 
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RESULT 12

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Page 5
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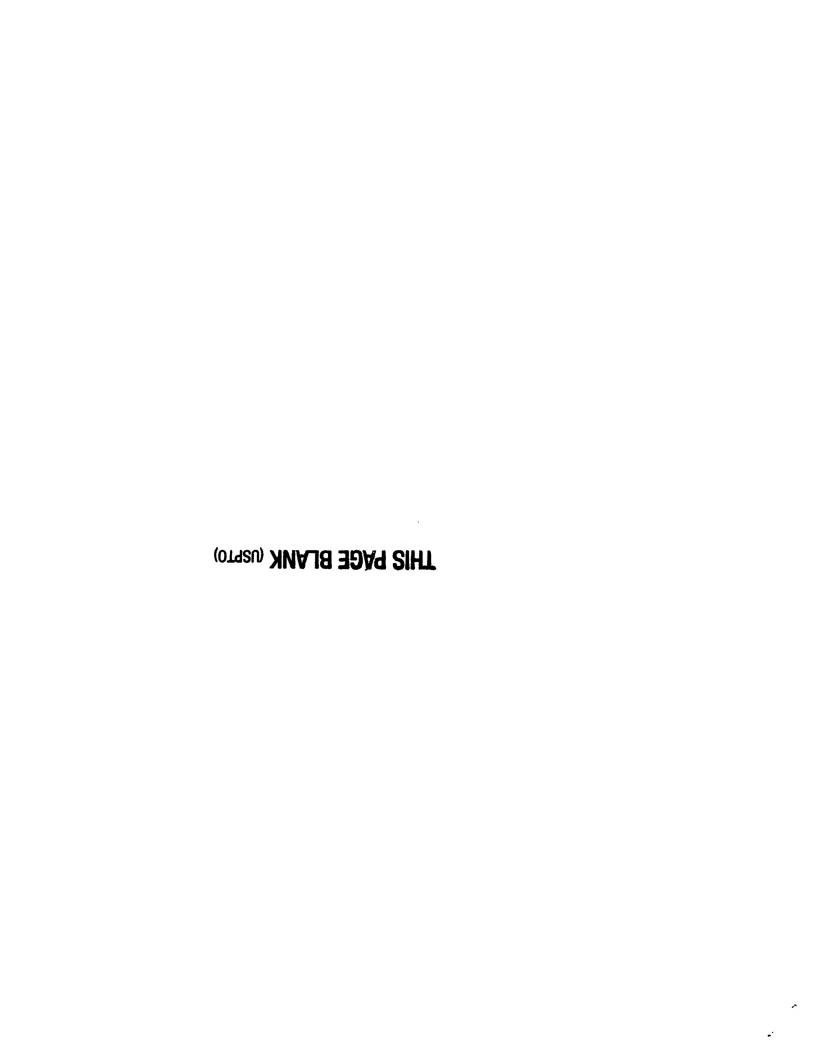
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us-10-614-959-15.rapb
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Mon Dec 5 16:39:23 2005

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US-10-293-418-1917

Query Match
Best Local Similarity 100.0%; Score 58; DB 15; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAWDDSLSEFL 11
Db 225 AAWDDSLSEFL 235
Search completed: October 14, 2005, 17:00:44
Job time: 78.2031 secs
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C007 %7:45:01 C

C83366 T40104 T40102 T40102 T40102 H84228 F84698 S23756 IVHOA1 IVHOA2 IVHOA3 IVHOA4 F81855 C98855

hypothetical prote conserved hypothet conserved hypothet thiamin biosynthes probable thiamin by probable PPE prote hypothetical prote CFTR protein - Afr interferon alpha-I insertion alement probable sugar tra hypothetical prote

6633.8 6633.8 6633.8 6633.8 6622.1 6621.1 6621.1 6621.1

October 14, 2005, 16:02:59 ; Search time 15.2969 Seconds (without alignments) 69.190 Million cell updates/sec

US-10-614-959-15 58 1 AAWDDSLSEFL 11

Title: Perfect score:

Sequence:

Scoring table:

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

using sw model

protein search,

OM protein

Run on:

ALIGNMENTS

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ig lambda chain pr
Ig lambda chain pr
Ig lambda chain vIg lambda cha \$36048 \$2750 \$18058 \$36046 \$11HUWA \$36046 \$11HUWA \$23626 \$23627 \$23757 \$25757 \$ Query Match Length DB 98 1129 95 95 1109 1109 4355 4855 4857 1110 1110 1300 4344 4444 Result

1 AAMDDSLS 8 |||||||| 90 AAWDDSLS 97

RESULT 2
S78058
G. Special and Descursor V-J region (clone mAB 67VL) - human (fragment)
G. Special Homo sapiens (man)
A. Reference number: S78051
A. Reference number: S78058
A. Molecule type: mRNA
A. Residues: 1-129
A. Residues: 1-129
A. Residues: 1-129
A. Residues: B. Man
A. Residues: B. Special Homo sapiens (man)
A. A. Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and his

A, Reference number: S23716; MUID: 92031262; PMID: 1718404

A;Accession: S23723
A;Molecule type: mRNA
A;Residues: 19-129 «HAM»
A;Kesidues: 19-129 «HAM»
A;Cross-references: EMBL:XA4446
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin (fragment) #status predicted <SIG>F;1-18/Domain: signal sequence (fragment)

Best Local Similarity 100. Matches 8; Conservative

Query Match

108 AAWDDSLS 115

Ig lambda chain - human

1 AAWDDSLS 8

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C)Accession: S49571
R)Giachino, C.; Padovan, E.; Lanzavecchia, A.
Submitted to the EMBL Data Library, November 1994
A;Description: k+1+ dual receptor B cells are present in the human peripheral repertoire.
A;Reference number: S49571
A;Accession: S49571
A;Accession: S49571
A;Accession: S49571
A;Residues: preliminary
A;Residues: 1-95
A;Cross-references: EMBL: Z46625; NID:g575259; PIDN: CAA866595.1; PID:g575260
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Ig lambda chain - human (fragment)

Ig lambda chain - human (fragment)

Ig lambda chain - human (fragment)

C;Species: Homo sapiens (man)

C;Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S36046

A;Reference number: S36046

A;Accession: S36046

A;Accession: S16046

A;Accession: I-98 **MIL>
A;Reference number: DNA

A;Cose-references: EMBL: Z22187; NID: G312312; PIDN: CAA80197.1; PID: G312313

C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C'Species: Homo sapiens (man)
C'Species: Homo sapiens (man)
C'Species: How-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C'Spacession: S36047
R'Williams, S.C.
Submitted to the EMBL Data Library, April 1993
A,Reference number: S36046
A,Reference number: S36047
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-98 «WIL-
A,Fresidues: 1-98 «WIL-
A,Cross-references: EMBL:Z22188; NID:G312291; PIDN:CAA80198.1; PID:G312292
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-91/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                  Ig lambda chain precursor V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
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Pred. No. 4.2;
1; Mismatches
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87.5%; Pred. No. 4.4;
cive 1; Mismatches
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Best Local Similarity 87.5
Matches 7; Conservative
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91 AAWDDSLDGYV 101
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76 AAWDDSLT 83
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Best Local Similarity
Matches 7; Conserv
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A,Gene: GDB:119342; OMIM:147240
A,Gene: GDB:120119342; OMIM:147240
A,Gene: GDB:12011.2-22411.2
C,Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c; Complex: An immunoglobulin heterotetramer subunit sand igm, the subunits associate into la c; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin V region; immunoglobulin; pyroglutamic acid
F;15-92/Domain: immunoglobulin homology <IMM>
F;15-92/Domain: immunoglobulin homology <IMM>
F;16-92/Domain: immunoglobulin pyroglutamic acid
F;22-90/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: A25479; D.P.; Congy, N.; Peran-Rivat, L.; Mihaesco, C.
R;Mihaesco, E.; Roy, J.P.; Congy, N.; Peran-Rivat, L.; Mihaesco, C.
Bur. J. Biochem. 150, 349-357, 1985
A;Title: The amino acid sequence of a lambda light chain presenting abnormal physicochem A;Reference number: A25479; MUID:85257662; PMID:2410269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: $22750
K;Combristo, G; Klobeck, H.G.
Rur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: $16439; MUID:91257162; PMID:1904362
A;Accession: $2550
A;Status: preliminary; translation not shown
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A;Note: residues 33-36 and some of the sequenced peptides were positioned by homology
C;Comment: The C region of this chain has the Mcg+ and Kern+ markers.
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C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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         F;19-129/Product: Ig lambda chain (fragment) #status predicted <MAT>F;33-109/Domain: immunoglobulin homology <IMM>
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Pred. No. 3.4;
2; Mismatches 2; Indels
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100.0%; Pred. No. 3.3;
ative 0; Mismatches
                                                                                                     DB 2;
                                                                                                  74.1%; Score 43; DB 100.0%; Pred. No. 1.7 tive 0; Mismatches
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Ig lambda chain V-I region (Mem) - human

A; Molecule type: protein A; Residues: 1-112 <MIH>

C; Genetics:

Query Match Best Local Similarity luv...

A; Residues: 1-235 < COM>

109 AAWDDSLS 116

g ઠ

1 AAWDDSLS 8

70.7%;

Query Match
Best Local Similarity 63.6
Matches 7; Conservative

8

|||||||: 109 AAWDDSLN 116

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C; Keywords: heterotetramer; immunoglobulin

Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative

ઠે g A; Cross-references: UNIPROT: P04208

C, Genetics:

A;Molecule type: protein A;Residues: 1-109 <TAK>

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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens
Airle: Genetic analyals of self-associating immunoglobulin G rheumatoid factors from to Airle: Genetic analyals of self-associating immunoglobulin G rheumatoid factors from to Airle: Genetic analyals of self-associating immunoglobulin G rheumatoid factors from to Airle: Genetic analyals
Airle: Genetic ana
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Daces: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25752
R;Combriato, G.; Klobeck, H.G.
R;Combriato, G.; Klobeck, H.G.
Rur. J. Immunol. 21, 1513-1522, 1991
A;Title: V[Jambda) and J(Jambda) -C(Jambda) gene segments of the human immunoglobulin lamb A;Reference number: S16439; MUID:91257162; PMID:1904362
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25757
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(Lambda) and J(lambda) -C(lambda) gene segments of the human immunoglobulin lamb
A;Reference number: S16439; MUID:91257162; PMID:1904362
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A;Rolecule type: mRNA
A;Rosidues: 1-233 <COM>
A;Residues: 1-233 <COM>
A;Cross-references: EMBL:X57817; NID:g33733; PIDN:CAA40954.1; PID:g33734
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>
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Pred. No. 6.9;
1; Mismatches
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Ig lambda chain V region - human (fragment)
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A;Molecule type: mRNA
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87.5%;
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Best Local Similarity 87.5
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Best Local Similarity 87.5
Matches 7; Conservative
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LI land sapiens (man) - human
C;Species: Homo sapiens (man)
C;Dete: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A01967
R;Takahashi, Y.; Takahashi, N.; Tetaert, D.; Putnam, F.W.
Proc. Natl. Acad. Sci. U.S.A. 80, 3686-3690, 1983
A;Title: Complete covalent structure of a human immunoglobulin D: sequence of the lambda
A;Reference number: A01967; MUID:83221661; PMID:6407018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: GDB:IGLV@
A;Gene: GDB:IJ9342; OMIM:147240
A;Cross-references: GDB:IJ9342; OMIM:147240
A;Cross-references: GDB:IJ9342; OMIM:147240
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamally: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;1-97/Region: V segment
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C;Species: Homo sapiens (man)
C;Accession: S23627
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
A;Colee, T.; Lu, E.W.; Hang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from the A;Reference number: S23623; MUID:92156804; PMID:1740665
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A;Molecule type: DNA
A;Residues: 1-117 <OLE>
A;Cross-references: EMBL;X59707; NID:g34426; PIDN:CAA42228.1; PID:g34427
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-110/Domain: immunoglobulin homology <IMM>
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       Length 98;
                                                                              0; Indels
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Score 40; DB 2;
Pred. No. 4.4;
1; Mismatches (
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Pred. No. 4.9;
0; Mismatches
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69.0%; Score 40; DB 2;
Best Local Similarity 87.5%; Pred. No. 5.3;
Matches 7; Conservative 1; Mismatches (
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F:22-89/Disulfide bonds: #status predicted
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69.0%; 80.0%;

Query Match
Best Local Similarity 80.0
Matches 8; Conservative

1 AAWDDSLSEF 10

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1 AAWDDSLS

A;Residues: 1-234 <COM>

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probable glycerol kinase (EC 2.7.1.30) [imported] - Sinorhizobium mellloti (strain 1021) C;Species: Sinorhizobium mellioti C;Species: Sinorhizobium mellioti C;Species: Sinorhizobium mellioti C;Species: Sinorhizobium mellioti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 C;Accession: G95983 R; Will and T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernand R; Proc. Natl. Accession: G95983 A;Accession: G95983 A;Accession: G95983 A;Accession: G95983 A;Accession: G95983 A;Status: prellminary A;Molecule type: DNA A;Accession: G95983 A;Status: prellminary A;Molecule type: DNA A;Residues: 1-497 ckUR. A;Residues: 1-497 ckU
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Best Local Similarity 70.0%;
Matches 7; Conservative
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C, Keywords: phosphotransferase
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession B87394
C;Accession B87394
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n. J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. W.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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A;Cross-references: UNIPROT:Q9A925; GB:AE005673; NID:g13422491; PIDN:AAK23153.1; GSPDB:C
C;Genetice
A;Gene: C21169
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R;Combriato, G.; Klobeck, H.G.
R;Title: Vlambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam A;Reference number: 816439; MUID:91257162; PMID:1904362
A;Recession: 825754
A;Recession: 825754
A;Recession: Preliminary; translation not shown
A;Residues: 1-235 <COM>
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C;Species: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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                                    A,Cross-references: EMBL:X57822; NID:g33743; PIDN:CAA40959.1; PID:g33744 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;149-217/Domain: immunoglobulin homology <IMM>
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Pred. No. 18;
1; Mismatches
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Pred, No. 11;
1; Mismatches
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87.5%;
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Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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SAWDDSLS 145
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S25754
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RESULT 15

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Gaps ö

Length 497; 2; Indels

Score 40; DB 2; Pred. No. 26; 1; Mismatches

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Copyright (c) 1993 - 2005 Compugen Ltd.	OM protein - protein search, using sw model	October 14, 2005, 15:51:44 ; Search time 73.2188 Seconds (without alignments) 76.932 Million cell updates/sec	US-10-614-959-15	: 58 1 AAWDDSLSEFL 11
Copyright	otein search	October 14,	US-10-614-9	1 AAWDDSLSE
	OM protein - pro	Run on:	Title:	Sequence:

Total number of hits satisfying chosen parameters:

1612378 segs, 512079187 residues

Searched:

Scoring table: BLOSUM62 Gapext 0.5

1612378

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	9968b0 homo sapien Q8nejl homo sapien Q6clt9 kluyvercmyc P06887 homo sapien Q6clt9 kluyvercmyc P06887 homo sapien Q6dhw4 homo sapien Q94208 homo sapien Q94208 homo sapien Q88205 caulobacter Q9jkl5 rattus norv Q9npf8 homo sapien Q8803 rhizobium m Q88904 microcystis Q09475 caenorhabdi P45443 neurospora Q673m1 homo sapien P24256 bos taurus Q873m1 homo sapien Q873m1 homo sapien Q8448 mericella Q739m0 mycobacter Q98tr8 bufo bufo Q6c0zl yarrowia li Q74b13 geobacter Q8544 emericella Q739c0 mycobacteri Q67np3 symbiobacte Q31358 bracillus ce Q72969 bacillus ce	Q815w5 bacillus ce
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Q81xi0 bacillus an Q6hbpl bacillus th Q74e50 geobacter 8 Q8pln5 xanthomonas Q09205 caenorhabdi Q9f6d9 streptomyce Q6r8a5 sholluscum c Q83155 molluscum c Q9b091 mycobacteri Q7wx48 nonomuraea Q9uwf6 candida alb P46005 escherichia P21672 saccharomyc	70	AA.	Ogosob; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 26, Last annotation update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Anti-streptococcal/anti-myosin immunoglobulin lambda light chain Homo sapiens (Human). Bukartyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homo sapiens (Human). ROBI TaxID=9606; NCEI TaxID=9606; NCEI TaxID=9606; NCEI TaxID=9606; NCEI TaxID=9606; NCEI TaxID=9808; NCEI TaxID=9808; NCEI TaxID=9808; NOSIDIRES-98375893; PubMed=9712075; Adderson B.E. Shikhman A.R., Ward K.E., Cunningham M.W.; Menderlar analysis of polyreactive monoclonal antibodies from antibody v region genes."; "Molecular analysis of polyreactive monoclonal antibodies from antibody v region genes."; "Molecular analysis of polyreactive monoclonal antibodies from antibody v region genes."; "Molecular analysis of polyreactive monoclonal antibodies from antibody v region genes."; "Molecular analysis of polyreactive monoclonal antibodies from antibody v region genes."; "Molecular analysis of polyreactive monoclonal antibodies from antibody v region genes."; "Molecular analysis of polyreactive monoclonal antibodies from antibody v region genes."; "Molecular analysis of polyreactive monoclonal antibodies from antibody v region genes."; "Molecular analysis of polyreactive monoclonal antibodies from antibody v region genes."; "Molecular analysis of polyreactive monoclonal antibodies from antibody v region genes."; "Molecular analysis of polyreactive monoclonal antibodies from
Q81XIO Q6HBP1 Q74BESO DAPA XANAC SRA3 CAEEL Q9F6D9 Q768A6 Q768A6 Q976S3 Q83155 Q98091 Q7WZ48 PLB1 CANAL AGGC_ECOLI	ALIGNMENTS	PRT; 108 AA	Created) Last sequence Last annotati in immunoglob Craniata; Craniata; Aard K.E., Ward K.E., ward K.E., reactive monoc tti-N-acetylgl Score 44; D Score 44; D
5.5 5.5 5.5 5.5 5.5 5.5 5.5 5.5		PRELIMINARY;	O956SB0; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MRR-2004 (TrEMBLrel. 26, Last annotation update) Anti-streptococcal/anti-myosin immunoglobulin lambda Anti-streptococcal/anti-myosin immunoglobulin lambda Homo sapiens (Human) Butable region (Fragment) Butaryota; Metazoa; Chordata; Catarrhini; Hominidae; NCBI TaxID=B606; NCBI TaxID=B606; NCBI TaxID=B606; NCBI TaxID=B606; Adderson B.E., Shikhman A.R., Ward K.E., Cunningham Manderson B.E., Shikhman A.R., Ward K.E., Cunningham Manderson B.E., Shikhman A.H., Wacetylglucosamine/an antibocallar analysis of polyreactive monoclonal antibo antibody vegion genes."; Mederson B.E., Shikhman A.H., Nacetylglucosamine/an antibody vegion genes."; Mederson Jeli2020-2031(1998). EMBL, USG394; AAB68783.1; EMBL, USG394; AAB68783.1; InterPro: IPR00710; 19-11ke. InterPro: IPR00710; 19-11ke. InterPro: IPR00710; 19-11ke. InterPro: IPR00710; 10-1164. SWART; SM0406; IGV; 1. SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64 ENGUENCE 108 AA; 11594 MW; F4B5DC478A043F48 LEAGTH
44444444444444444444444444444444444444	LT 1	96SB0	Q965B0; O1-DEC-2001 (TYEMBLEE1.1 O1-DEC-2001 (TYEMBLEE1.1 O1-MAR-2004 (TYEMBLEE1.2 Antl-streptcocccal/antl-m variable region (Fragment Homo sapiens (Human). NCBI_TAXID=9606; SEQUENCE FROM N.A. MEDLINE=98375893; PubMed= Adderson B.E., Shikhman A. MOBCULER analysis of porheumatic carditis: human antibody V region genes." J. Immunol. 161:2020-2031 EMBL; U96394; AAB68783.1; EMBL; U96394; AAB68783.1; InterPro; IPR00310; IG-1 InterPro; IPR003596; IG-Y SMART; SM00406; IGV; I PROSITE; PS50835; IG-LIKE NON_TER 1 SEQUENCE 108 AA; 11594
	RESULT	OSSSO OI O	PAC DE DE PETE SE

Gaps ô 2; Indels Pred. No. 3.1; 1; Mismatches Best Local Similarity 72.7%; Matches 8; Conservative ઠે 셤

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OBNEJ1 PRELIMINARY; PRT; 236 AA.
OBNEJ1;
OBNEJ1;
OLOCT-2002 (TERBLrel. 22, Last sequence update)
O1-OCT-2002 (TERBLrel. 26, Last annotation update)
O1-MAR-2004 (TERBLrel. 26, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Home saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. RESULT 2
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RP [1]
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[1] -SEQUENCE FROM N.A. TISSUE=Lung;

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Query Match
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              Rausnesez, 300.27; Frunredel.44, 173.2; DOL=10.10/3/pnas.44603899;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
A Hopkins R.F., Jordan H., Poore T., Max S.I., Wang J., Heieh F.,
A Hopkins R.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Uadin T.B., Toehiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Weckrnan K.J., Malek J.A., Gunaratne P.H.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Soderige B.J., Lu X., Gibbs R.A.,
A Holton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones S.J., Maria M.A.;
Jones S.J., Maria M.A.;
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T. D. C., Maria D.N., Sold C., Shard L.J., L., L., C., Colly full-length human
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Despons L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
Similar to sployHFC6 Yarrowia lipolytica Calnexin.
ORFNames=KLLA0F00462g; P. 1140.
Bukaryota; Fungl; Saccharomycetaceae; Kluyveromycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC0309984; AAH30984.1; -.
HSSP; P01703; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASSEPTOTION (TABLE):
InterPro): IPR007110; Ig-like.
InterPro): IPR003597; Ig_c1.
InterPro): IPR003596; Ig_WHC.
InterPro): IPR003596; Ig_V.
Pfam; PF07654; C1-8et; 1.
SWART; SW00406; IGV; 1.
PROSITE; PS00299; IG_MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 236 AA; 25024 MW; 1703B77942630E08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.1%; Score 43; DB 2;
100.0%; Pred. No. 11;
rative 0; Mismatches C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=284590;
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Mihaesco E., Roy J.P., Congy N., Peran-Rivat L., Mihaesco C., "The amino acid sequence of a lambda light chain presenting abnormal physicochemical and antigenic features.";

Bur. J. Blochem. 150:349-357(1985).

-I. MISCELLANEOUS: Residues 33-36 and some of the sequenced peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                were positioned by homology.
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Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A., Jancher C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J. Wincker P., Souciet J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
Monoclonal antibody; Prrolidone carboxylic acid.
DOMAIN
MOD RES 1 1 Pyrrolidone carboxylic acid.
MOD RES 1 By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 2; Length 628;
Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                               Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                         EMBL, CR382126; CAG97807.1; -..
GO, GO:0005514; F:calcium ion storage activity; IEA.
GO, GO:0005514; F:calcium ion storage activity; IEA.
InterPro; IPR001580; Calret/Calnex.
InterPro; Oral alike_lec_gl.
Pfan, PP00262; Calreticulin, 1.
PRINTS; PR00626; CALRETICULIN.
PROSITE; P800803; CALRETICULIN 1; 1.
PROSITE; P800803; CALRETICULIN 1; 1.
SEQUENCE 628 AA; 70981 MW; B0DBA6D1A6464EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1. SIMILARITY: Contains 1 immunoglobulin-like domain. PIR; A25479; LiHUVM.
HSSP; PO1703; 7FAB.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0003823; F:antigen binding; NAS.
InterPro: IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
10 lambda chain V-I region MEM.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
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MEDLINE=85257662; PubMed=2410269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 66.7
tes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 WDDSISEYI 317
                                                                                                                                                                                                                     Nature 430:35-44(2004)
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                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A.
STRAIN=NRRL Y-1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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P06887;
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||||||:| 109 AAWDDSMS 116

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112 AA; 11789 MW; 748124F079CFFBE4 CRC64;

SEQUENCE Query Match

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C007 \$7:66.01 C

SEQUENCE FROM N.A.
STRAINS-ATCC 19089 / CB15;
MEDLINE-21173698, Pubmed=11259647; DOI=10.1073/pnas.061029298;
MEDLINE-21173699, Pubmed=11259647; DOI=10.1073/pnas.061029298;
Mierman W.C., Felddhyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Perocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B. DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J., White O., Salzberg S.L., Venter J.C., Shapiro L., Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Caulobacter. (VGI_TaxID=155892; 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein CC1169. Caulobacter crescentus Query Match RESULT 6 LV1F HUMAN Q9A925 RESULT 7 Q9A925 ò TISSUE=Primary B-Cells;

TISSUE=Primary B-Cells;

X MEDILNE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.P., Gares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Hownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Brownstein M.J., Wodin T.B., Toshiyuki S., Carninci P., Prange C.,

R Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

R Allakesley R.W., Touchman M., Madan A., Rodrigues S., Sanchez A.,

R Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

R Rodriguez A.C., Grimwood J., Schwurtz J., Myers R.M., Butterffield Y.S.,

R Jones S.J., Marra M.A.,

A Jones S.J., Marra M.A.,

R Generation and initial analysis of more than 15,000 full-length human and monaton and manneaus and manneaus and monaton and manneaus and manneaus and monaton and manneaus and manneaus and monaton and manneaus and monaton and manneaus and monaton and manneaus and manneaus and manneaus and monaton and manneaus and manneaus and monaton and manneaus and manneaus and manneaus and manneaus and ö ö Gaps Gaps Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606, ö ö A Straubberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; ROO7843; AAH75843.1; -.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR003599; Ig-cl.
R InterPro; IPR003599; Ig-cl.
R InterPro; IPR003599; Ig-cl.
R InterPro; IPR003596; Ig-WHC.
R InterPro; IPR003596; Ig-WHC.
R EMBR; SMO0409; IG; 2.
SMART; SMO0409; IG; 2.
SMART; SMO0409; IG; 2.
R SMART; SMO0406; IGv; 1.
R SMART; SMO0406; IG MHC; UNKNOWN_1. / Match 10.7%; Score 41; DB 1; Length 112; Local Similarity 63.6%; Pred. No. 12; 17; Conservative 2; Mismatches 2; Indels 70.7%; Score 41; DB 2; Length 237; 87.5%; Pred. No. 26; 0; Indels rative 1; Mismatches 0; Indels 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
4 (TrEMBLrel. 28, Last annotation update)
4 (Mono sapiens (Human).
5 (Mono sapiens Morror). roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) 237 AA PRELIMINARY; 91 AAWDDSLDGYV 101 and mouse cDNA sequences. Best Local Similarity 87.5 Matches 7; Conservative 1 AAWDDSLSEFL 11 TISSUE=Primary B-Cells; SEQUENCE FROM N.A. Q6DHW4 Q6DHW4; Matches RESULT 5
066HW4
1D Q60H
AC Q6DH
AC Q6DH
AC Q6DH
AC G6DH
CS-0
DT 25-0
DT 26-0
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PRELIMINARY;

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Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
Takahashi Y., Takahashi N., Tetaert D., Putnam famunoglobulin D: sequence of the lambda light chain.";
The lambda light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 AA; 11725 MW; B17785F6A8DF9BAC CRC64;
                                                                  20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ig lambda chain V-I region WAH.
               109 AA
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By similarity.
           PRT;
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       STANDARD;
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89
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LV1F HUMAN P04208;
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NON TER
SEQUENCE
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1 AAWDDSLS

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Pfam; PF01412; ArfGap; 1.
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Mittley P., Gibbard A.M., Koumanov F., Oldfield S., Kilgour E.E.,
Mittley P., Gibbard A.M., Koumanov F., Oldfield S., Kilgour E.E.,
Mittley P., Gibbard A.M., Koumanov F., Oldfield S., Kilgour E.E.,
M. Prestation of centaurin-alpha2: a phosphatidylinositide-binding
T. Drotein present in fat, heart and skeletal muscle.";
Eur. J. Cell Biol. 81:22-220 (2002).

C. I- FUNCTION: Greacactivating protein for the ADP ribosylation
factor family (Potential).

C. I- SUBUNIT: Binds phosphatidylinositol 4.5-bisphosphate,
phosphatidylinositol 3.4,5-terisphosphate (PtdInsP3) and inositol
J.3.4,5-terakisphosphate (InsP4). Binding of phosphatidylinositol
J.3.4,5-terakisphosphate (InsP4). Binding of phosphatidylinositol
J.3.4,5-terakisphosphate (InsP4). Binding of phosphatidylinositol
J.3.4,5-terakisphosphate and phosphatidylinositol J., Stateman in Cartions
J.S. Shipphosphate and phosphatidylinositol J., Stateman Lower affinity. Opossesse a stoichlometry of two binding
sites for InsP4 with identical affinity (By similarity).

C. I- SUBCELTULAR LOCATION: Expressed in many tissues, with highest levels
T. TISSUE SPECIFICITY: Expressed in many tissues, with highest levels
T. TISSUE SPECIFICITY: Expressed in many tissues, with highest levels
T. TISSUE ADD TANDER TO THE TO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@18b-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., INTERACTION WITH PTDINS(4,5)P2, FTDINS(3,4,5)P3
AND INS(1,3,4,5)P4, TISSUE SPECIFICITY, AND MUTAGENESIS OF ARG-151 AND
ARG-275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                       Length 355;
                                                                                                                                                                                                                                                Indels
             "Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
EMBL, AE005795; AAK23153.1; -.
PIR; E87394; -.
                                                                                                        Interproj Formal Luciferase like.
Interproj IRPO1251; Luciferase like.
Pfam; PF00296; Bac luciferase; I.
Complete proteome; Hypothetical protein.
SEQUENCE 355 AA; 38552 MW; 3C4AEF42825E5567 CRC64;
                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                       Score 40; DB 2;
Pred. No. 63;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-00T-2004 (Rel. 45, Created)
25-00T-2004 (Rel. 45, Last sequence update)
25-00T-2004 (Rel. 45, Last annotation update)
Centaurin alpha 2.
                                                                                                                                                                                                                                                                                                                                                                                                                   376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and lung.
-!- SIMILARITY: Contains 1 Arf-GAP domain.
-!- SIMILARITY: Contains 2 PH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001164; hRIP_like.
InterPro; IPR001849; PH.
InterPro; IPR011036; PH_related.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ238993; CAB88403.1; -.
                                                                                                                                                                                                             69.0%;
                                                                                                                                                                                            Query Match
Best Local Similarity 87.5
7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGD; 708487; LOC56826
                                                                                                                                                                                                                                                                                                                        138 SAWDDSLS 145
                                                                                                                                                                                                                                                                                       œ
                                                                                                                                                                                                                                                                                         1 AAWDDSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Adipocyte;
     Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
CEA2_RAT
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         RAT REL DR DR DR KY RAY SQ KW
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TISSUB=Leukocyte;
MEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hateh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownerein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=20104757; PubMed=10843809; DOI=10.1006/geno.2000.6179;
Jenne D.E., Tingchert S., Stegmann B., Reimann H., Nurnberg P.,
Horn D., Naumann I., Buske A., Thiel G.;
"A common set of a Least 11 functional genes is lost in the majority
of NF1 patients with gross deletions.";
Genomics 66:93-97(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=22012451; PubMed=12018390;
Whitley P., Gibbard A.M., Koumanov F., Oldfield S., Kilgour E.E.,
Prestwich G.D., Holman G.D.;
"Identification of centamin-alpha2: a phosphatidylinositide-binding
protein present in fat, heart and skeletal muscle.";
Eur. J. Cell Biol. 81:222-230(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                          R->C: Almost complete loss of InsP4 binding.
R->C: Oloss of InsP4 binding. Almost complete loss of InsP4 binding; when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                 GTPage activation; Metal-binding; Repeat; Zinc; Zinc-finger. DOMAIN 9 130 Arf-GAP. ZN FING 25 48 C4-type. DOMAIN 131 232 PH 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 1; Length 376;
Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
Bertsch U., Illies C., Mayr G.W.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                            376 AA; 43524 MW; B357392F38F07166 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CEA2_HUMAN STANDARD; PRT; 381 AA. 09NPF8; 08M406; 096SD5; 28-FBB-2003 (Rel. 41, Created) 25-FBB-2003 (Rel. 41, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Centaurin alpha 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                             C4-type.
PH 1.
PH 2.
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Pfam; PF00169; PH; 2.
PRINTS, PR00405; REVINTRACTNG.
SMART; SM00105; ArfGap; 1.
SMART; SM00233; PH; 2.
PROSITE; PS50115; ARFGAP; 1.
PROSITE; PS50003; PH_DOWAIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 69.0%;
Similarity 66.7%;
6; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                             131
254
151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                      MUTAGEN
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                                                                                                                                                                                                                                                                                              DOMAIN
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CEA2_HUMAN
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Page
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us-10-614-959-15.rup

COO7 47.60.07 C

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu K., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Grhen E.J., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences."

INTERACTION WITH PTDINS(3,4,5)P3 AND INS(1,3,4,5)P4, TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
PubMed=14690521;

Hanck T., Stricker R., Sedehizade F., Reiser G., Indentification of gene structure and subcellular localization of human centaurin alpha 2, and p42IP4, a family of two highly homologous, Ins 1,3,4,5-P4-/PtdIns 3,4,5-P3-binding, adapter

proteins.",
J. Neurochem. 88:326-336(2004).
-!- FUNCTION: GTPasse-activating protein for the ADP ribosylation
-!- FUNCTION: GTPasse-activating protein for the ADP ribosylation
-!- SUBUNIT: Binds phosphatedylinositol 3,4,5-trisphosphate (PtdInsP3)
and inositol 1,3,4,5-tetrakisphosphate (InsP4). Possesses a
stoichiometry of two binding sites for InsP4 with identical

affinity.
SUBCELLULAR LOCATION: Cytoplasmic. Constitutively associated with the plasma membrane. Excluded from the nucleus.
ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2; Name=1;

IsoId=Q9NPF8-1; Sequence=Displayed;

Isold=O9NPPB-2; Sequence=VSP_011180;
Note=May be due to a competing acceptor splice site. No
experimental confirmation available;
-1- TISSUE SPECIFICITY: Highly expressed in placenta, spleen, kidney,
skeletal muscle and adrenal gland. Weakly expressed in thyroid,
liver, heart, lung, small intestine, peripheral blood leukocytes.
Not detected in spinal cord, brain, stomach, trachea, colon, lymph
node and bone marrow.
-1- SIMILARITY: Contains 1 Arf-GAP domain.

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EMBL, AJ238994; CAB88383.1; -.
EMBL; AJ272195; CAB7266.1; -.
EMBL; BAJ242782; CAC46651.1; -.
EMBL; BC033758; AA43758.1; -.
Genew; HGNC:16487; CENTA2.
HINDB; HIX0013699; -.
MIM; 608635; -.
InterPro; IPR001164; hRIP_like.
InterPro; IPR001164; PH.
InterPro; IPR001186; PH.

Pfam; PF01412; Arfcap; T.
Pfam; PF00169; PH; 2.
PRINTS; PR00405; REVINTRACING.
SMART; SM0105; ArfGap; 1.
SMART; SM00233; PH; 2.

PROSITE; PS50115; ÄRFGAP; 1. PROSITE; PS50003; PH DOMAIN; 2. Alternative splicing; GTPase activation; Metal-binding; Repeat; Zinc; Zinc-finger.

Gapa ö Query Match 69.0%; Score 40; DB 1; Length 381; Best Local Similarity 66.7%; Pred. No. 68; Matches 6; Conservative 2; Mismatches 1; Indels Arf-GAP.
C4-type.
PH 1.
PH 2.
Missing (in isoform 2).
/Frid=VSP_011180. 3 WDDSLSEFL 11 25 132 255 269 DOMAIN ZN_FING DOMAIN DOMAIN CONFLICT SHIFFFF ઠ

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||||: ||: 69 WDDSIVEFM 77

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RN SEQUENCE FROM N.A.

RC STRAIN=FVB/N, TISSUE=Breast tumor;

RX MEDLINE-21388627; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE-22388627; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Altaeberg R.L., Feligodd E.A., Grouse L.H., Derge J.G.

RA Alteschul S.P., Zeeberg B., Bustow K.H., Schaefer C.P., Bhat N.K.,

RA Hopkins R.P., Jordan H., Moore T., Maxs J.I., Haich F. N.

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldow M.P., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loguellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

RA Raha S.S., Loguellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glubs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glubs R.A.,

RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Muting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Muting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C. Grimwood J., Schmutz J., Myers R.M.,

Bakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RY Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002)

C. -- FUNCTION: GTPase-activating protein for the ADP ribosylation

factor family (Potential).

C. -- SUBUNT: Binds phosphatidylinostcol 3.4.5-trisphosphate (PtdInsP3)

and inositol 1.3.4.5-tetrakisphosphate (InsP4). Possesses a

stcickhomercry of two binding sites for InsP4 with identical

affinity (By similarity).

C. -- SUBUNT: Contains 1 Arth Gamain.

C. -- SIMILARITY: Contains 1 Arth Gamain.

C. -- SIMILARITY: Contains 1 Arth Gamain. Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090; 25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Centaurin alpha 2. PRT; 381 AA STANDARD; Name=Centa2; MOUSE RESULT 10 CEA2_MOUSE ID CEA2_MOU AC QBR2V5;

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MEDLINE=99121023; PubMed=9922248;
Medline=9922248;
Medline=992248;
Medline=992248;
Medline=992248;
Medline=992248;
Medline=992248;
Medline=992248;
Medline=992248;
Medline=99
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16-OCT-2001 (Rel. 40, Last sequence update)
15-OCT-2004 (Rel. 45, Last annotation update)
Glycerol kinase (EC 2.7.1.30) (AFP:glycerol 3-phosphotransferase)
(Glycerokinase) (GK).
                                                     | MODING | M
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--- PATHARY: Glycerol utilization; rate-limiting step.
--- SIMILARIY: Belongs to the fucckinase / gluconokinase / glycerokinase / xylulokinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=glpK; OrderediocusNames=RB1135; ORFNames=SMb21009; Rhizobium meliloti (Sinorhizobium meliloti). Plasmid pSymB (megaplasmid 2). Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium. NRBI_TAXID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     metabolism.
-!- CATALYTIC ACTIVITY: ATP + glycerol = ADP + sn-glycerol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 66.7%; Score 40; DB 1; Length 381; 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2E504CEF0ACD84D5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C4-type.
PH 1.
PH 2.
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255 361 PF
381 AA; 43989 MW;
                            EMBL; BC027165; AAH27165.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 WDDSLSEFL 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                EMBL; ALS91985; CAC49535.1; -.
EMBL; AP080548; AAD12735.1; -.
EMBL; AP080548; AAD12735.1; -.
HNSP; P08859; 1GLG.
HAMAP; MF_00186; -; 1.
InterPro; IPR000579; Glycerol_kin.
InterPro; IPR00599; Glycerol_kin.
Pfam; PF02782; FGGY_C; 1.
Pfam; PF02782; FGGY_N; 1.
Pfam; PF0370; FGGY_N; 1.
PROSITE; PS00933; FGGY_KINASES_1; FALSE_NEG.
PROSITE; PS00445; FGGY_KINASES_2; 1.
ATP-binding; Complete proteome; Glycerol metabolism; Kinase; Plasmid;
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                                                                                                                                                                                                                                                                                                                                                               69.0%; Score 40; DB 1; Length 497; 70.0%; Pred. No. 90; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=HUB 5-2-4;
Juerchoct K., Boerner T.;
Juerchoct K., Boerner T.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; 228337; CAA82191.1; -.
PIR; 549113; S49113.
InterPro; IPR0007936; CytC_heme_BS.
InterPro; IPR0007936; VirE.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                    153 165 ATP (Probable).
497 AA, 54419 MW; 42D3428335ACC2B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Cyanobacteria; Chroococcales; Microcystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
201-NOV-1995 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Putative helicase C28H8.3 (EC 3.6.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1714 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         502 AA
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nes 6; Conservative
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AWDDSLSEFL 11
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YP93_CAEEL
ID YP93_CAEEL
AC Q09475;
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Q48904;
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Matches
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Q48904
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ORFNames=C28H8.3;

18-10-614-959-15.rup

SIMILARITY: Belongs to the dynein heavy chain family. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). Caenorhabditis elegans. Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. Waterston R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: Belongs to the helicase family. SKI2 subfamily. STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
The C. elegans sequencing consortium;
Genome sequence of the nematode C. elegans: a platform for investigating biology.";
Science 282:2012-2018(1998). 69.0%; Score 40; DB 1; Length 1714; 88.9%; Pred. No. 3.4e+02; tive 0; Mismatches 1; Indels EMBL, U20861; AAA62291.2;

WormBase; WBGene00016194; C28H8.3.

WormPep; C28H8.3; CE29195.

InterPro; IPR00140; DBEAD.

InterPro; IPR001650; Helicase_C.

Ffam; PF00270; Helicase_C; 1.

SNART; SM00490; HELICc; 1.

SNART; SM00490; HELICc; 1.

TIGRFAMS; TIGR01870; cas_TM1810; 2.

ATP-binding; Helicase; Hydrolase; Hypothetical protein;

Nuclear protein.

Nuclear protein.

NP BIND 607 614 ATP (Potential).

NP BIND 806 813 ATP (Potential).

SITE 607 614 ATP (Potential). 806 813 ATP (Potential). 813 916 DEVH box. 1714 AA, 194095 MW, 0936764D27C7EFAD CRC64, Local Similarity 88.5 NCBI_TaxID=6239; SEQUENCE FROM N.A. [2] REVISIONS. SEQUENCE Query Match

ö Gaps STRAIN=74-0R23-1M. / FGSC 987; MEDLINE=95014704; PubMed=7929559; DOI=10.1083/jcb.127.1.139; Plamann M., Minke P.F., Tinsley J.H., Bruno K.S.; "Cytoplasmic dynein and actin-related protein Arp1 are required for DYACCAR STANDARD; PRT; 4367 AA.
P45443; Q7RVH1;
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUJ-2004 (Rel. 44, Last annotation update)
Dynein heavy chain, cytosolic (DYHC).
Name=ro-1; ORFNames=NCU06976.1;
Name=ro-1; ORFNames=NCU06976.1;
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora. ô . 5 AAWDDSDSE 13 1 AAWDDSLSE 9 SEQUENCE FROM N.A.

DYHC_NEUCR

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PARAINE-TO-CAUGATA FGGS 987;

RE STRAINE-T-OR23-1187; DOI=0.0198/nature01554;

RE Debede=12712197; DOI=0.0198/nature01554;

RA BAINE T. Edulos S.B., Borkovich K.A., Selker E.U., Read N.D.,

Aglagan J.E., Calvo S.B., Borkovich K.A., Selker E.U., Read N.D.,

Alting T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,

RA BIKING T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,

RA Dui D., Inankiev P., Bell-Pedersen D., Nelson M.A.,

Rambarer Washburne M., Seltremnikoff C.P., Kinsey J.A., Braun E.L.,

Rampage-Thomann N., Barrett R., Grerre S., Kamal M., Kamvyssells M.,

Rampage-Thomann N., Barrett R., Grein M., S., Cogoni C.,

Rampagen C.P., Glass L., Orbach M.J., Berglund J.A., Voelker R.,

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Rampagen C.P., Glass L., Orbach M.J., Berglund J.A., Voelker R.,

Rampagen I., Sachs M.S., Lander E.S., Dunlap J., Rredford A., Aramayo R.,

Ruter 422.859-868(2003).

-I-FUNCTION: Cytoplasmic dynein acts as a motor for the intracellular retrograde motility of vesicles and organelles along microtubules Dynein has Arpase activity; the force-producing power stroke is thought to occur on release of ADP. Required to maintain uniform nuclear distribution in hyphae.

-I-FUNCTION: Consists of at least two heavy chains and a number of throught brinds cargo and light chains:

-I-FUNCTION: Consists of at least two heavy chains and a number of threath and the head or micro domain. The motor contains six tandemly—

-I-MOMAIN: Dynain heavy chains probably conist of an N-terminal strengen of the head or rmal nuclear distribution in filamentous fungi."; Cell Biol. 127:139-149(1994). N.A.

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DR EMBL, L31504; AAA64908.1; -..

DR EMBL, AABX01000204; EAA33380.1; -..

DR InterPro; IPR003264; EAA33380.1; -..

DR InterPro; IPR003264; Danain heavy.

DR InterPro; IPR003269; AAA ATPase.

DR MART; SM00382; AAA, 3.

KW ATP-binding; Coiled coil; Dynein; Microtubule; Motor protein; Repeat.

FT DOWAIN 1905 2130 AAA 1 (By similarity).

FT DOWAIN 2506 2816 AAA 1 (By similarity).

FT DOWAIN 2506 2816 AAA 4 (By similarity).

FT DOWAIN 3193 3481 Stah (By similarity).

FT DOWAIN 3193 3481 Stah (By similarity).

FT DOWAIN 3156 3794 AAA 5 (By similarity).

FT DOWAIN 3155 Coiled coil (Potential).

176 1215 Coiled coil (Potential).

1351 Coiled coil (Potential).

6 33 S

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Pred. No. 9.3e+02;
2; Mismatches 1; Indels
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MW; 1E10F3E2D170D6DF CRC64;
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3778 3809
1943 2247
2605 2617 2547
4367 AA, 495568 MV
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Best Local Similarity 66.7%;
Matches 6; Conservative
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